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<110> EDWARDS, ALED DHARAMSI, AKIL VEDADI, MASOUD ALAM, MUHAMMAD ZAHOOR DOMAGALA, MEGAN HOUSTON, SIMON LAM, ROBERT LI, QIN NETHERY, KATHLEEN NG, IVY PINDER, BENJAMIN VIOLA, CRISTINA WREZEL, OLGA KANAGARAJAH, DHUSHY MANSOURY, KAMRAN NECAKOV, ALEKSANDAR SASHA VALLEE, FRANCOIS MCDONALD, MERRY-LYNN

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Leu Ser Lys Leu Gly Ala Asn Val Thr Val Asn Asp Gly Lys Asp Leu 35 40 45

Ser Gln Asp Ala His Ala Lys Asp Leu Glu Ser Met Gly Ile Ser Val
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Val Ser Gly Ser His Pro Leu Thr Leu Leu Asp Asn Asn Pro Ile Ile 65 70 75 80

Val Lys Asn Pro Gly Ile Pro Tyr Thr Val Ser Ile Ile Asp Glu Ala 85 90 95

Val Lys Arg Gly Leu Lys Ile Leu Thr Glu Val Glu Leu Ser Tyr Leu 100 105 110

Ile Ser Glu Ala Pro Ile Ile Ala Val Thr Gly Thr Asn Gly Lys Thr 115 120 125

Thr Val Thr Ser Leu Ile Gly Asp Met Phe Lys Lys Ser Arg Leu Thr 130 140

Gly Arg Leu Ser Gly Asn Ile Gly Tyr Val Ala Ser Lys Val Ala Gln 145 150 155 160

Glu Val Lys Pro Thr Asp Tyr Leu Val Thr Glu Leu Ser Ser Phe Gln 165 170 175

Leu Leu Gly Ile Glu Lys Tyr Lys Pro His Ile Ala Ile Ile Thr Asn 180 185 190

Ile Tyr Ser Ala His Leu Asp Tyr His Glu Asn Leu Glu Asn Tyr Gln
195 200 205

Asn Ala Lys Lys Gln Ile Tyr Lys Asn Gln Thr Glu Glu Asp Tyr Leu 210 215 220 Ile Cys Asn Tyr His Gln Arg Gln Val Ile Glu Ser Glu Glu Leu Lys 225 230 235 240

Ala Lys Thr Leu Tyr Phe Ser Thr Gln Gln Glu Val Asp Gly Ile Tyr
245 250 255

Ile Lys Asp Gly Phe Ile Val Tyr Lys Gly Val Arg Ile Ile Asn Thr
260 265 270

Glu Asp Leu Val Leu Pro Gly Glu His Asn Leu Glu Asn Ile Leu Ala 275 280 285

Ala Val Leu Ala Cys Ile Leu Ala Gly Val Pro Ile Lys Ala Ile Ile 290 295 300

Asp Ser Leu Thr Thr Phe Ser Gly Ile Glu His Arg Leu Gln Tyr Val 305 310 315 320

Gly Thr Asn Arg Thr Asn Lys Tyr Tyr Asn Asp Ser Lys Ala Thr Asn 325 330 335

Thr Leu Ala Thr Gln Phe Ala Leu Asn Ser Phe Asn Gln Pro Ile Ile 340 345 350

Trp Leu Cys Gly Gly Leu Asp Arg Gly Asn Glu Phe Asp Glu Leu Ile 355 360 365

Pro Tyr Met Glu Asn Val Arg Ala Met Val Val Phe Gly Gln Thr Lys 370 375 380

Ala Lys Phe Ala Lys Leu Gly Asn Ser Gln Gly Lys Ser Val Ile Glu 385 390 395 400

Ala Asn Asn Val Glu Asp Ala Val Asp Lys Val Gln Asp Ile Ile Glu 405 410 415

Pro Asn Asp Val Val Leu Leu Ser Pro Ala Cys Ala Ser Trp Asp Gln
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Ser Gln Asp Ala His Ala Lys Asp Leu Glu Ser Met Gly Ile Ser Val
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Val Ser Gly Ser His Pro Leu Thr Leu Leu Asp Asn Asn Pro Ile Ile 65 70 75 80

Val Lys Asn Pro Gly Ile Pro Tyr Thr Val Ser Ile Ile Asp Glu Ala 85 90 95

Val Lys Arg Gly Leu Lys Ile Leu Thr Glu Val Glu Leu Ser Tyr Leu 100 105 110

Ile Ser Glu Ala Pro Ile Ile Ala Val Thr Gly Thr Asn Gly Lys Thr 115 120 125

Thr Val Thr Ser Leu Ile Gly Asp Met Phe Lys Lys Ser Arg Leu Thr 130 135 140

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Glu Val Lys Pro Thr Asp Tyr Leu Val Thr Glu Leu Ser Ser Phe Gln 165 170 175

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 195 200 205
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- Ala Val Leu Ala Cys Ile Leu Ala Gly Val Pro Ile Lys Ala Ile Ile 290 295 300
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- Thr Leu Ala Thr Gln Phe Ala Leu Asn Ser Phe Asn Gln Pro Ile Ile 340 345 350
- Trp Leu Cys Gly Gly Leu Asp Arg Gly Asn Glu Phe Asp Glu Leu Ile 355 360 365
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Ala Leu Arg Asn Lys Gly Ile Lys Ile Leu Pro Phe Asp Ala Asn Asn
                         55
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Ser Arg Thr Gln Ala Phe Leu Asn Glu Phe Ala Glu Ser Leu Ser Lys 355 360 365

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gcacaccatc caagagaaat tagtgctaca attgaaacag cacgaaagaa atatccacat 1020
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gaatttgcag aaagtttaag taaagcagat cgtgtattct tatgtgaaat ttttqqatca 1140
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tegttaatta atgaagatte tattaatgta ttagaacaat ttgataatge tgttatttta 1260
tttatgggtg caggtgatat tcaaaaatta caaaatgcat atttagataa attaggcatg 1320
aaaaatgcgt tttaa
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<211> 444
<212> PRT
<213> Staphylococcus aureus
<400> 30
Met Ser Lys Glu Phe Tyr Ile Met Thr His Tyr His Phe Val Gly Ile
Lys Gly Ser Gly Met Ser Ser Leu Ala Gln Ile Met His Asp Leu Gly
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25

20

- His Glu Val Gln Gly Ser Asp Ile Glu Asn Tyr Val Phe Thr Glu Val
 35 40 45
- Ala Leu Arg Asn Lys Gly Ile Lys Ile Leu Pro Phe Asp Ala Asn Asn 50 55 60
- Ile Lys Glu Asp Met Val Val Ile Gln Gly Asn Ala Phe Ala Ser Ser 65 70 75 80
- His Glu Glu Ile Val Arg Ala His Gln Leu Lys Leu Asp Val Val Ser 85 90 95
- Tyr Asn Asp Phe Leu Gly Gln Ile Ile Asp Gln Tyr Thr Ser Val Ala
 100 105 110
- Val Thr Gly Ala His Gly Lys Thr Ser Thr Thr Gly Leu Leu Ser His 115 120 125
- Val Met Asn Gly Asp Lys Lys Thr Ser Phe Leu Ile Gly Asp Gly Thr 130 135 140
- Tyr Arg Arg His Phe Leu Ser Tyr Lys Pro Asp Tyr Ala Ile Met Thr 165 170 175
- Asn Ile Asp Phe Asp His Pro Asp Tyr Phe Lys Asp Ile Asn Asp Val 180 185 190
- Phe Asp Ala Phe Gln Glu Met Ala His Asn Val Lys Lys Gly Ile Ile 195 200 205
- Ala Trp Gly Asp Asp Glu His Leu Arg Lys Ile Glu Ala Asp Val Pro 210 215 220
- Ile Tyr Tyr Tyr Gly Phe Lys Asp Ser Asp Asp Ile Tyr Ala Gln Asn 225 230 235 240
- Ile Gln Ile Thr Asp Lys Gly Thr Ala Phe Asp Val Tyr Val Asp Gly 245 250 255
- Glu Phe Tyr Asp His Phe Leu Ser Pro Gln Tyr Gly Asp His Thr Val 260 265 270
- Leu Asn Ala Leu Ala Val Ile Ala Ile Ser Tyr Leu Glu Lys Leu Asp 275 280 285
- Val Thr Asn Ile Lys Glu Ala Leu Glu Thr Phe Gly Gly Val Lys Arg 290 295 300
- Arg Phe Asn Glu Thr Thr Ile Ala Asn Gln Val Ile Val Asp Asp Tyr 305 310 315 320
- Ala His His Pro Arg Glu Ile Ser Ala Thr Ile Glu Thr Ala Arg Lys 325 330 335

пуъ	ıyı	Pro	340	гÀг	GIU	vai	vaı	345	vai	Pne	Gin	Pro	350	Thr	Pne		
Ser	Arg	Thr 355	Gln	Ala	Phe	Leu	Asn 360	Glu	Phe	Ala	Glu	Ser 365	Leu	Ser	Lys		
Ala	Asp 370	Arg	Val	Phe	Leu	Cys 375	Glu	Ile	Phe	Gly	Ser 380	Ile	Arg	Glu	Asn		
Thr 385	Gly	Ala	Leu	Thr	Ile 390	Gln	Asp	Leu	Ile	Asp 395	Lys	Ile	Glu	Gly	Ala 400		
Ser	Leu	Ile	Asn	Glu 405	Asp	Ser	Ile	Asn	Val 410	Leu	Glu	Gln	Phe	Asp 415	Asn		
Ala	Val	Ile	Leu 420	Phe	Met	Gly	Ala	Gly 425	Asp	Ile	Gln	Lys	Leu 430	Gln	Asn		
Ala	Tyr	Leu 435	Asp	Lys	Leu	Gly	Met 440	Lys	Asn	Ala	Phe						
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gcgg			atato	gacag	gt at	taad	cagat	t aaa	agtag	J						37	
<210 <211 <212 <213	> 36 > DN	i A	lcial	. Sec	quenc	ce											•
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<400 gcgc			taaa	ıcaat	a to	ccaaa	accad	c cga	aatg							36	
<210: <211: <212: <213:	> 35 > DN	IA.	.cia]	. Sec	quenc	ce											
<220: <223:	> De	scri		on of	Art	ific	cial	Sequ	ience	e: Sy	nthe	etic					

geggeggee atatgaagga gttttatata atgae	35
<210> 34 <211> 37 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic primer	
<400> 34 gcggcggccc atatgtttta tataatgaca cactatc	37
<210> 35 <211> 37 <212> DNA <213> Artificial Sequence	
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<210> 36 <211> 34 <212> DNA <213> Artificial Sequence	
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<210> 37 <211> 37 <212> DNA <213> Artificial Sequence	
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<400> 37 gcggcggccc atatgtatca ttttgtcgga attaaag	37

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<210> 38
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<223> Description of Artificial Sequence: Synthetic
      primer
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<211> 33
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic
      primer
<400> 39
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                                                                    33
<210> 40
<211> 43
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 40
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<210> 41
<211> 37
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 41
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<210> 42
<211> 37
<212> DNA
<213> Artificial Sequence
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<213> Staphylococcus aureus
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<210> 44
<211> 13
<212> PRT
<213> Staphylococcus aureus
<400> 44
Lys Ala Asp Arg Val Phe Leu Cys Glu Ile Phe Gly Ser
                  5
<210> 45
<211> 19
<212> PRT
<213> Staphylococcus aureus
<400> 45
Asp His Thr Val Leu Asn Ala Leu Ala Val Ile Ala Ile Ser Tyr Leu
                 5
Glu Lys Leu
<210> 46
<211> 924
<212> DNA
<213> Staphylococcus aureus
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gttgatgaac ctttaaaacg atacacttat actaaaacag gtggtaatgc cgacttttac 120
attaccccta ctaaaaatga agaagtacaa gcagttgtta aatatgccta tcaaaatgag 180
attcctgtta catatttagg aaatggctca aatattatta tccgtgaagg tggtattcgc 240
ggtattgtaa ttagtttatt atcactagat catatcgaag tatctgatga tgcgataata 300
gccggtagcg gcgctgcaat tattgatgtc tcacgtgttg ctcttgatta cgcacttact 360
ggccttgaat ttgcatgtgg tattccaggt tcaattggtg gtgcagtgta tatgaatgct 420
ggcgcttatg gtggcgaagt taaagattgt atagactatg cgctttgcgt aaacgaacaa 480
ggctcgttaa ttaaacttac aacaaaagaa ttagagttag attatcgtaa tagcattatt 540
caaaaagaac acttagttgt attagaagct gcatttactt tagctcctgg taaaatgact 600
gaaatacaag ctaaaatgga tgatttaaca gaacgtagag aatctaaaca acctttagag 660
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tatccttcat gtggtagtgt attccaaaga ccgcctggtc attttgcagg taaattgata 720 caagattcta atttgcaagg tcaccgtatt ggcggcgttg aagtttcaac caaacacgct 780 ggttttatgg taaatgtaga caatggaact gctacagatt atgaaaacct tattcattat 840 gtacaaaaga ccgtcaaaga aaaatttggc attgaattaa atcgtgaagt tcgcattatt 900 ggtgaacatc caaaggaatc gtaa 924 <210> 47

<211> 307

<212> PRT

<213> Staphylococcus aureus

<400> 47

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Glu Lys Ile Lys Val Asp Glu Pro Leu Lys Arg Tyr Thr Tyr Thr Lys
20 25 30

Thr Gly Gly Asn Ala Asp Phe Tyr Ile Thr Pro Thr Lys Asn Glu Glu 35 40 45

Val Gln Ala Val Lys Tyr Ala Tyr Gln Asn Glu Ile Pro Val Thr 50 55 60

Tyr Leu Gly Asn Gly Ser Asn Ile Ile Ile Arg Glu Gly Gly Ile Arg
65 70 75 80

Gly Ile Val Ile Ser Leu Leu Ser Leu Asp His Ile Glu Val Ser Asp 85 90 95

Asp Ala Ile Ile Ala Gly Ser Gly Ala Ala Ile Ile Asp Val Ser Arg 100 105 110

Val Ala Leu Asp Tyr Ala Leu Thr Gly Leu Glu Phe Ala Cys Gly Ile 115 120 125

Pro Gly Ser Ile Gly Gly Ala Val Tyr Met Asn Ala Gly Ala Tyr Gly 130 140

Gly Ser Leu Ile Lys Leu Thr Thr Lys Glu Leu Glu Leu Asp Tyr Arg 165 170 175

Asn Ser Ile Ile Gln Lys Glu His Leu Val Val Leu Glu Ala Ala Phe 180 185 190

Thr Leu Ala Pro Gly Lys Met Thr Glu Ile Gln Ala Lys Met Asp Asp 195 200 205

Leu Thr Glu Arg Arg Glu Ser Lys Gln Pro Leu Glu Tyr Pro Ser Cys 210 215 220

Gly Ser Val Phe Gln Arg Pro Pro Gly His Phe Ala Gly Lys Leu Ile 225 230 235 240

Gln Asp Ser Asn Leu Gln Gly His Arg Ile Gly Gly Val Glu Val Ser Thr Lys His Ala Gly Phe Met Val Asn Val Asp Asn Gly Thr Ala Thr Asp Tyr Glu Asn Leu Ile His Tyr Val Gln Lys Thr Val Lys Glu Lys 280 285 Phe Gly Ile Glu Leu Asn Arg Glu Val Arg Ile Ile Gly Glu His Pro 295 Lys Glu Ser <210> 48 <211> 924 <212> DNA <213> Staphylococcus aureus <400> 48 gtgataaata aagacatcta tcaagcttta caacaactta tcccaaatga aaaaattaaa 60 gttgatgaac ctttaaaacg atacacttat actaaaacag gtggtaatgc cgacttttac 120 attaccccta ctaaaaatga agaagtacaa gcagttgtta aatatgccta tcgaaatgag 180 attcctgtta catatttagg aaatggctca aatattatta tccgtgaagg tggtattcgc 240 ggtattgtaa ttagtttatt accactagat catatcgaag tatctgatga tgcgataata 300 gccggtagcg gcgctgcaat tattgatgtc tcacgtgttg ctcgtgatta cgcacttact 360 ggccttgaat ttgcatgtgg tattccaggt tcaattggtg gtgcagtgta tatgaatgct 420 ggcgcttatg gtggcgaagt taaagattgt atagactatg cgctttgcgt aaacgaacaa 480 ggctcgttaa ttaaacttac aacaaaagaa ttagagttag attatcgtaa tagcattatt 540 caaaaagaac acttagttgt attagaagct gcatttactt tagctcctgg taaaatgact 600 gaaatacaag ctaaaatgga tgatttaaca gaacgtagag aatctaaaca acctttagag 660 tatccttcat gtggtagtgt attccaaaga ccgcctggtc attttgcagg taaattgata 720 caagattcta atttgcaagg tcaccgtatt ggcggcgttg aagtttcaac caaacacgct 780 ggttttatgg taaatgtaga caatggaact gctacagatt atgaaaacct tattcattat 840 gtacaaaaga ccgtcaaaga aaaatttggc attgaattaa atcgtgaagt tcgcattatt 900 ggtgaacatc caaaggaatc gtaa <210> 49 <211> 307 <212> PRT <213> Staphylococcus aureus <400> 49 Val Ile Asn Lys Asp Ile Tyr Gln Ala Leu Gln Gln Leu Ile Pro Asn Glu Lys Ile Lys Val Asp Glu Pro Leu Lys Arg Tyr Thr Tyr Thr Lys Thr Gly Gly Asn Ala Asp Phe Tyr Ile Thr Pro Thr Lys Asn Glu Glu Val Gln Ala Val Val Lys Tyr Ala Tyr Arg Asn Glu Ile Pro Val Thr

Tyr Leu Gly Asn Gly Ser Asn Ile Ile Ile Arg Glu Gly Gly Ile Arg
65 70 75 80

Gly Ile Val Ile Ser Leu Leu Pro Leu Asp His Ile Glu Val Ser Asp 85 90 95

Asp Ala Ile Ile Ala Gly Ser Gly Ala Ala Ile Ile Asp Val Ser Arg
100 105 110

Val Ala Arg Asp Tyr Ala Leu Thr Gly Leu Glu Phe Ala Cys Gly Ile 115 120 125

Pro Gly Ser Ile Gly Gly Ala Val Tyr Met Asn Ala Gly Ala Tyr Gly 130 135 140

Gly Ser Leu Ile Lys Leu Thr Thr Lys Glu Leu Glu Leu Asp Tyr Arg 165 170 175

Asn Ser Ile Ile Gln Lys Glu His Leu Val Val Leu Glu Ala Ala Phe 180 185 190

Thr Leu Ala Pro Gly Lys Met Thr Glu Ile Gln Ala Lys Met Asp Asp 195 200 205

Leu Thr Glu Arg Arg Glu Ser Lys Gln Pro Leu Glu Tyr Pro Ser Cys 210 215 220

Gly Ser Val Phe Gln Arg Pro Pro Gly His Phe Ala Gly Lys Leu Ile 225 230 235 240

Gln Asp Ser Asn Leu Gln Gly His Arg Ile Gly Gly Val Glu Val Ser 245 250 255

Thr Lys His Ala Gly Phe Met Val Asn Val Asp Asn Gly Thr Ala Thr 260 265 270

Asp Tyr Glu Asn Leu Ile His Tyr Val Gln Lys Thr Val Lys Glu Lys 275 280 285

Phe Gly Ile Glu Leu Asn Arg Glu Val Arg Ile Ile Gly Glu His Pro 290 295 300

Lys Glu Ser 305

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<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

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<210> 51
<211> 37
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
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                                                                   37
<210> 52
<211> 8
<212> PRT
<213> Staphylococcus aureus
<400> 52
Val Gln Ala Val Val Lys Tyr Ala
                 5
<210> 53
<211> 14
<212> PRT
<213> Staphylococcus aureus
<400> 53
Val Lys Asp Cys Ile Asp Tyr Ala Leu Cys Val Asn Glu Gln
<210> 54
<211> 52
<212> PRT
<213> Staphylococcus aureus
<400> 54
Arg Gly Ile Val Ile Ser Leu Leu Ser Leu Asp His Ile Glu Val Ser
Asp Asp Ala Ile Ile Ala Gly Ser Gly Ala Ala Ile Ile Asp Val Ser
             20
                                 25
                                                      30
Arg Val Ala Leu Asp Tyr Ala Leu Thr Gly Leu Glu Phe Ala Cys Gly
Ile Pro Gly Ser
     50
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<210> 55

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<211> 921
<212> DNA
<213> Staphylococcus aureus
<400> 55
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gttacatttg gagagcctgc tattgcagta ccgtttaacg caggtaaaat caaagtttta 120
atagaagcct tagagagcgg gaactattcg tctattaaaa gcgatgttta cgatggtatg 180
ttatatgatg cgcctgacca tcttaagtct ttggtgaacc gttttgtaga attaaataat 240
attacagage egetageagt aaegateeaa aegaatttae caccateaeg tggattagga 300
tcgagtgcag ctgtcgcggt tgcttttgtt cgtgcaagtt atgatttttt agggaaatca 360
ttaacgaaag aagaactcat tgaaaaggct aattgggcag agcaaattgc acatggtaaa 420
ccaagtggta ttgatacgca aacgattgta tcaggcaaac cagtttggtt ccaaaaaggt 480
catgctgaaa cgttgaaaac gttaagttta gacggctata tggttgttat agatactggt 540
gtgaaaggtt caacaagaca agcagtagaa gatgttcata aactttgtga ggaccctcag 600
tacatgtcac atgtaaaaca tatcggtaag ttagttttac gtgcgagtga tgtgattgaa 660
catcataact ttgaagcctt agcggatatt tttaatgaat gtcatgcgga tttaaaggcg 720
ttgacagtta gtcatgataa aatagaacaa ttaatgaaaa ttggtaaaga aaatggtgcg 780
attgctggaa aacttactgg cgctggtcgt ggtggaagta tgttattgct tgccaaagat 840
ttaccaacag cgaaaaatat tgtaaaagct gtagaaaaag ctggtgcagc acatacttgg 900
attgagaatt taggaggtta a
<210> 56
<211> 306
<212> PRT
<213> Staphylococcus aureus
<400> 56
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Gly Glu His Ala Val Thr Phe Gly Glu Pro Ala Ile Ala Val Pro Phe
             20
Asn Ala Gly Lys Ile Lys Val Leu Ile Glu Ala Leu Glu Ser Gly Asn
                             40
Tyr Ser Ser Ile Lys Ser Asp Val Tyr Asp Gly Met Leu Tyr Asp Ala
Pro Asp His Leu Lys Ser Leu Val Asn Arg Phe Val Glu Leu Asn Asn
Ile Thr Glu Pro Leu Ala Val Thr Ile Gln Thr Asn Leu Pro Pro Ser
Arg Gly Leu Gly Ser Ser Ala Ala Val Ala Val Ala Phe Val Arg Ala
                                105
                                                    110
Ser Tyr Asp Phe Leu Gly Lys Ser Leu Thr Lys Glu Glu Leu Ile Glu
                            120
Lys Ala Asn Trp Ala Glu Gln Ile Ala His Gly Lys Pro Ser Gly Ile
    130
                        135
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Asp Thr Gln Thr Ile Val Ser Gly Lys Pro Val Trp Phe Gln Lys Gly
145
                    150
His Ala Glu Thr Leu Lys Thr Leu Ser Leu Asp Gly Tyr Met Val Val
Ile Asp Thr Gly Val Lys Gly Ser Thr Arg Gln Ala Val Glu Asp Val
            180
                                185
His Lys Leu Cys Glu Asp Pro Gln Tyr Met Ser His Val Lys His Ile
Gly Lys Leu Val Leu Arg Ala Ser Asp Val Ile Glu His His Asn Phe
Glu Ala Leu Ala Asp Ile Phe Asn Glu Cys His Ala Asp Leu Lys Ala
                    230
                                        235
Leu Thr Val Ser His Asp Lys Ile Glu Gln Leu Met Lys Ile Gly Lys
                                    250
Glu Asn Gly Ala Ile Ala Gly Lys Leu Thr Gly Ala Gly Arg Gly Gly
Ser Met Leu Leu Ala Lys Asp Leu Pro Thr Ala Lys Asn Ile Val
Lys Ala Val Glu Lys Ala Gly Ala Ala His Thr Trp Ile Glu Asn Leu
                        295
                                            300
Gly Gly
305
<210> 57
<211> 921
<212> DNA
<213> Staphylococcus aureus
<400> 57
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gttacatttg gagagcctgc tattgcagta ccgtttaacg caggtaaaat caaagtttta 120
atagaageet tagagagegg gaactatteg tetattaaaa gegatgttta egatggtatg 180
ttatatgatg cgcctgacca tcttaagtct ttggtgaacc gttttgtaga attaaataat 240
attacagage egetageagt aaegatecaa aegaatttac caccateaeg tggattagga 300
tcgagtgcag ctgtcgcggt tgcttttgtt cgtgcaagtt atgatttttt agggaaatca 360
ttaacgaaag aagaactcat tgaaaaggct aattgggcag agcaaattgc acatggtaaa 420
ccaagtggta ttgatacgca aacgattgta tcaggcaaac cagtttggtt ccaaaaaggt 480
catgctgaaa cgttgaaaac gttaagttta gacggctata tggttgttat agatactggt 540
gtgaaagggt caacaagaca agcagtagaa gatgttcata aactttgtga ggaccctcag 600
tacatgtcac atgtaaaaca tatcggtaag ttagttttac gtgcgagtga tgtgattgaa 660
catcataact ttgaagcctt agcggatatt tttaatgaat gtcatgcgga tttaaaggcg 720
ttgacagtta gtcatgataa aatagaacaa ttaatgaaaa ttggtaaaga aaatggtgcg 780
attgctggaa aacttactgg cgctggtcgt ggtggaagta tgttattgct tgccaaagat 840
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attgagaatt taggaggtta a

- <210> 58
- <211> 306
- <212> PRT
- <213> Staphylococcus aureus
- <400> 58
- Met Thr Arg Lys Gly Tyr Gly Glu Ser Thr Gly Lys Ile Ile Leu Ile 1 5 10 15
- Gly Glu His Ala Val Thr Phe Gly Glu Pro Ala Ile Ala Val Pro Phe 20 25 30
- Asn Ala Gly Lys Ile Lys Val Leu Ile Glu Ala Leu Glu Ser Gly Asn 35 40 45
- Tyr Ser Ser Ile Lys Ser Asp Val Tyr Asp Gly Met Leu Tyr Asp Ala
 50 55 60
- Pro Asp His Leu Lys Ser Leu Val Asn Arg Phe Val Glu Leu Asn Asn 65 70 75 80
- Ile Thr Glu Pro Leu Ala Val Thr Ile Gln Thr Asn Leu Pro Pro Ser 85 90 95
- Arg Gly Leu Gly Ser Ser Ala Ala Val Ala Val Ala Phe Val Arg Ala
 100 105 110
- Ser Tyr Asp Phe Leu Gly Lys Ser Leu Thr Lys Glu Glu Leu Ile Glu 115 120 125
- Lys Ala Asn Trp Ala Glu Gln Ile Ala His Gly Lys Pro Ser Gly Ile 130 135 140
- Asp Thr Gln Thr Ile Val Ser Gly Lys Pro Val Trp Phe Gln Lys Gly 145 150 155 160
- His Ala Glu Thr Leu Lys Thr Leu Ser Leu Asp Gly Tyr Met Val Val
 165 170 175
- Ile Asp Thr Gly Val Lys Gly Ser Thr Arg Gln Ala Val Glu Asp Val
 180 185 190
- His Lys Leu Cys Glu Asp Pro Gln Tyr Met Ser His Val Lys His Ile 195 200 205
- Gly Lys Leu Val Leu Arg Ala Ser Asp Val Ile Glu His His Asn Phe 210 215 220
- Glu Ala Leu Ala Asp Ile Phe Asn Glu Cys His Ala Asp Leu Lys Ala 225 230 235 240
- Leu Thr Val Ser His Asp Lys Ile Glu Gln Leu Met Lys Ile Gly Lys 245 250 255
- Glu Asn Gly Ala Ile Ala Gly Lys Leu Thr Gly Ala Gly Arg Gly Gly 260 265 270

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Ser Met Leu Leu Ala Lys Asp Leu Pro Thr Ala Lys Asn Ile Val
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                                      285 .
Lys Ala Val Glu Lys Ala Gly Ala Ala His Thr Trp Ile Glu Asn Leu
Gly Gly
305
<210> 59
<211> 33
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
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<400> 59
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<210> 60
<211> 34
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
     primer
<400> 60
gcgcggatcc cggctctgta atattattta attc
                                                                 34
<210> 61
<211> 20
<212> PRT
<213> Staphylococcus aureus
<400> 61
Ser Ser Ala Ala Val Ala Val Ala Phe Val Arg Ala Ser Tyr Asp Phe
                                   10
Leu Gly Lys Ser
            20
<210> 62
<211> 16
<212> PRT
<213> Staphylococcus aureus
<400> 62
Thr Leu Lys Thr Leu Ser Leu Asp Gly Tyr Met Val Val Ile Asp Thr
                                    10
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<210> 63
<211> 21
<212> PRT
<213> Staphylococcus aureus
<400> 63
Tyr Met Ser His Val Lys His Ile Gly Lys Leu Val Leu Arg Ala Ser
                                     10
Asp Val Ile Glu His
            2.0
<210> 64
<211> 960
<212> DNA
<213> Escherichia coli
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catcgtctgc gtgaaaaaag cgtagaactg acacgtaaaa tcttcgccga tctcggtgca 180
tggcagattg cgcaactggc acgccatcca cagcgtcctt ataccctgga ttacgttcgc 240
ctggcatttg atgaatttga cgaactggct ggcgaccgcg cgtatgcaga cgataaagct 300
atcgtcggtg gtatcgcccg tctcgatggt cgtccggtga tgatcattgg tcatcaaaaa 360
ggtcgtgaaa ccaaagaaaa aattcgccgt aactttggta tgccagcgcc agaaggttac 420
cgcaaagcac tgcgtctgat gcaaatggct gaacgcttta agatgcctat catcaccttt 480
atcgacaccc cgggggctta tcctggcgtg ggcgcagaag agcgtggtca gtctgaagcc 540
attgcacgca acctgcgtga aatgtctcgc ctcggcgtac cggtagtttg tacggttatc 600
ggtgaaggtg gttctggcgg tgcgctggcg attggcgtgg gcgataaagt gaatatgctg 660
caatacagca cctattccgt tatctcgccg gaaggttgtg cgtccattct gtggaagagc 720
gccgacaaag cgccgctggc ggctgaagcg atgggtatca ttgctccgcg tctgaaagaa 780
ctgaaactga tcgactccat catcccggaa ccactgggtg gtgctcaccg taacccggaa 840
gcgatggcgg catcgttgaa agcgcaactg ctggcggatc tggccgatct cgacgtgtta 900
agcactgaag atttaaaaaa tcgtcgttat cagcgcctga tgagctacgg ttacgcgtaa 960
<210> 65
<211> 319
<212> PRT
<213> Escherichia coli
<400> 65
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                 5
Ala Lys Ile Asp Ser Leu Thr Ala Val Ser Arg Gln Asp Glu Lys Leu
Asp Ile Asn Ile Asp Glu Glu Val His Arg Leu Arg Glu Lys Ser Val
Glu Leu Thr Arg Lys Ile Phe Ala Asp Leu Gly Ala Trp Gln Ile Ala
Gln Leu Ala Arg His Pro Gln Arg Pro Tyr Thr Leu Asp Tyr Val Arg
                    70
                                         75
```

Leu Ala Phe Asp Glu Phe Asp Glu Leu Ala Gly Asp Arg Ala Tyr Ala 85 90 95

Asp Asp Lys Ala Ile Val Gly Gly Ile Ala Arg Leu Asp Gly Arg Pro
100 105 110

Val Met Ile Ile Gly His Gln Lys Gly Arg Glu Thr Lys Glu Lys Ile 115 120 125

Arg Arg Asn Phe Gly Met Pro Ala Pro Glu Gly Tyr Arg Lys Ala Leu 130 135 140

Arg Leu Met Gln Met Ala Glu Arg Phe Lys Met Pro Ile Ile Thr Phe 145 150 155 160

Ile Asp Thr Pro Gly Ala Tyr Pro Gly Val Gly Ala Glu Glu Arg Gly 165 170 175

Gln Ser Glu Ala Ile Ala Arg Asn Leu Arg Glu Met Ser Arg Leu Gly 180 185 190

Val Pro Val Val Cys Thr Val Ile Gly Glu Gly Gly Ser Gly Gly Ala 195 200 205

Leu Ala Ile Gly Val Gly Asp Lys Val Asn Met Leu Gln Tyr Ser Thr 210 215 220

Tyr Ser Val Ile Ser Pro Glu Gly Cys Ala Ser Ile Leu Trp Lys Ser 225 230 235 240

Ala Asp Lys Ala Pro Leu Ala Ala Glu Ala Met Gly Ile Ile Ala Pro 245 250 255

Arg Leu Lys Glu Leu Lys Leu Ile Asp Ser Ile Ile Pro Glu Pro Leu 260 265 270

Gly Gly Ala His Arg Asn Pro Glu Ala Met Ala Ala Ser Leu Lys Ala 275 280 285

Gln Leu Leu Ala Asp Leu Ala Asp Leu Asp Val Leu Ser Thr Glu Asp 290 295 300

Leu Lys Asn Arg Arg Tyr Gln Arg Leu Met Ser Tyr Gly Tyr Ala 305 310 315

<210> 66

<211> 960

<212> DNA

<213> Escherichia coli

<400> 66

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ategteggtg gtategeeg tetegatggt egteeggtga tgateattgg teateaaaaa 360 ggtegtgaaa ccaaagaaaa aattegeegt aactttggta tgeeageec agaaggttac 420 egeaaageac tgegtetgat geaaatgget gaaegettta agatgeetat cateacettt 480 ategacacec egggggetta teetggegtg ggegeagaag agegtggtea gtetgaagee 540 attgeaegea acetgegtga aatgtetege eteggegtac eggtagtttg taeggttate 600 ggtgaaggtg gteetggegg tgegetggeg attggegtgg gegataaagt gaatatgeeg 660 eaatacagea eetatteegt tatetegeeg gaaggttgtg eggeeaatet tgggaaagag 720 geegacaaag egeegetgge ggetgaageg atgggtatea ttgeteegeg tetgaaagaa 780 etgaaactga tegaeteea eateeeggaa eeactgggtg gtgeteaeeg taaeeeggaa 840 gegatggeeg eategttgaa agegeaactg etggeggate tggeegatet eggeegtta 900 ageaettgaa atttaaaaaa tegtegttat eagegeetga taagetaegg ttaeegegtaa 960

<210> 67

<211> 319

<212> PRT

<213> Escherichia coli

<400> 67

Met Ser Leu Asn Phe Leu Asp Phe Glu Gln Pro Ile Ala Glu Leu Glu
1 5 10 15

Ala Lys Ile Asp Ser Leu Thr Ala Val Ser Arg Gln Asp Glu Lys Leu 20 25 30

Asp Ile Asn Ile Asp Glu Glu Val His Arg Leu Arg Glu Lys Ser Val 35 40 45

Glu Leu Thr Arg Lys Ile Phe Ala Asp Leu Gly Ala Trp Gln Ile Ala 50 60

Gln Leu Ala Arg His Pro Gln Arg Pro Tyr Thr Leu Asp Tyr Val Arg 65 70 75 80

Leu Ala Phe Asp Glu Phe Asp Glu Leu Ala Gly Asp Arg Ala Tyr Ala 85 90 95

Asp Asp Lys Ala Ile Val Gly Gly Ile Ala Arg Leu Asp Gly Arg Pro 100 105 110

Val Met Ile Ile Gly His Gln Lys Gly Arg Glu Thr Lys Glu Lys Ile 115 120 125

Arg Arg Asn Phe Gly Met Pro Ala Pro Glu Gly Tyr Arg Lys Ala Leu 130 135 140

Arg Leu Met Gln Met Ala Glu Arg Phe Lys Met Pro Ile Ile Thr Phe 145 150 155 160

Ile Asp Thr Pro Gly Ala Tyr Pro Gly Val Gly Ala Glu Glu Arg Gly
165 170 175

Gln Ser Glu Ala Ile Ala Arg Asn Leu Arg Glu Met Ser Arg Leu Gly
180 185 190

Val Pro Val Val Cys Thr Val Ile Gly Glu Gly Gly Ser Gly Gly Ala 195 200 205

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Leu Ala Ile Gly Val Gly Asp Lys Val Asn Met Leu Gln Tyr Ser Thr
                        215
Tyr Ser Val Ile Ser Pro Glu Gly Cys Ala Ser Ile Leu Trp Lys Ser
                    230
Ala Asp Lys Ala Pro Leu Ala Ala Glu Ala Met Gly Ile Ile Ala Pro
                                     250
                245
Arg Leu Lys Glu Leu Lys Leu Ile Asp Ser Ile Ile Pro Glu Pro Leu
Gly Gly Ala His Arg Asn Pro Glu Ala Met Ala Ala Ser Leu Lys Ala
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Gln Leu Leu Ala Asp Leu Ala Asp Leu Asp Val Leu Ser Thr Glu Asp
                        295
Leu Lys Asn Arg Arg Tyr Gln Arg Leu Met Ser Tyr Gly Tyr Ala
                    310
<210> 68
<211> 37
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 68
gcggcggccc atatgagtct gaatttcctt gattttg
                                                                   37
<210> 69
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     primer
<400> 69
gcgcggatcc atcaaatgcc aggcgaacg
                                                                   29
<210> 70
<211> 11
<212> PRT
<213> Escherichia coli
Arg Leu Gly Val Pro Val Val Cys Thr Val Ile
                 5
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<210> 71
<211> 21
<212> PRT
<213> Escherichia coli
<400> 71
Ala Ala Ser Leu Lys Ala Gln Leu Leu Ala Asp Leu Ala Asp Leu Asp
Val Leu Ser Thr Glu
             20
<210> 72
<211> 30
<212> PRT
<213> Escherichia coli
<400> 72
Phe Ala Asp Leu Gly Ala Trp Gln Ile Ala Gln Leu Ala Arg His Pro
Gln Arg Pro Tyr Thr Leu Asp Tyr Val Arg Leu Ala Phe Asp
<210> 73
<211> 945
<212> DNA
<213> Staphylococcus aureus
<400> 73
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gaacgagaaa ctaaaaaaat atatacaaat ctaaaaccat gggatcgtgt gcaaattgcg 180
cgtttgcaag aaagacctac gaccctagat tatattccat atatctttga ttcgtttatg 240
gaactacatg gtgatcgtaa ttttagagat gatccagcaa tgattggtgg tattggcttt 300
ttaaatggtc gtgctgttac agttattgga caacaacgtg gaaaagatac aaaagataat 360
atttatcgaa attttggtat ggcgcatcca gaaggttatc gaaaagcatt acgtttaatg 420
aaacaagctg aaaaattcaa tcgtcctatc tttacattta tagatacaaa aggtgcatat 480
cctggtaaag ctgctgaaga acgtggacaa agtgaatcta tcgcaacaaa tttgattgag 540
atggcttcat taaaagtacc agttattgcg attgtcattg gtgaaggtgg cagtggaggt 600
gctctaggta ttggtattgc caataaagta ttgatgttag agaatagtac ttactctgtt 660
atatctcctg aaggtgcagc ggcattatta tggaaagaca gtaatttggc taaaattgca 720
gctgaaacaa tgaaaattac tgcccatgat attaagcaat taggtattat agatgatgtc 780
atttctgaac cacttggcgg tgcacataaa gatattgaac agcaagcttt agctattaaa 840
tcagcgtttg ttgcacagtt agattcactt gagtcattat cacgtgatga aattgctaat 900
gatcgctttg aaaaattcag aaatatcggt tcttatatag aataa
                                                                   945
<210> 74
<211> 314
<212> PRT
<213> Staphylococcus aureus
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- <400> 74
- Met Leu Asp Phe Glu Lys Pro Leu Phe Glu Ile Arg Asn Lys Ile Glu 1 5 10 15
- Ser Leu Lys Glu Ser Gln Asp Lys Asn Asp Val Asp Leu Gln Glu Glu 20 25 30
- Ile Asp Met Leu Glu Ala Ser Leu Glu Arg Glu Thr Lys Lys Ile Tyr 35 40 45
- Thr Asn Leu Lys Pro Trp Asp Arg Val Gln Ile Ala Arg Leu Gln Glu 50 55
- Arg Pro Thr Thr Leu Asp Tyr Ile Pro Tyr Ile Phe Asp Ser Phe Met 65 70 75 80
- Glu Leu His Gly Asp Arg Asn Phe Arg Asp Asp Pro Ala Met Ile Gly 85 90 95
- Gly Ile Gly Phe Leu Asn Gly Arg Ala Val Thr Val Ile Gly Gln Gln
 100 105 110
- Arg Gly Lys Asp Thr Lys Asp Asn Ile Tyr Arg Asn Phe Gly Met Ala 115 120 125
- His Pro Glu Gly Tyr Arg Lys Ala Leu Arg Leu Met Lys Gln Ala Glu 130 135 140
- Lys Phe Asn Arg Pro Ile Phe Thr Phe Ile Asp Thr Lys Gly Ala Tyr 145 150 155 160
- Pro Gly Lys Ala Ala Glu Glu Arg Gly Gln Ser Glu Ser Ile Ala Thr 165 170 175
- Asn Leu Ile Glu Met Ala Ser Leu Lys Val Pro Val Ile Ala Ile Val 180 185 190
- Ile Gly Glu Gly Ser Gly Gly Ala Leu Gly Ile Gly Ile Ala Asn 195 200 205
- Lys Val Leu Met Leu Glu Asn Ser Thr Tyr Ser Val Ile Ser Pro Glu 210 215 220
- Gly Ala Ala Ala Leu Leu Trp Lys Asp Ser Asn Leu Ala Lys Ile Ala 225 230 235 240
- Ala Glu Thr Met Lys Ile Thr Ala His Asp Ile Lys Gln Leu Gly Ile 245 250 255
- Ile Asp Asp Val Ile Ser Glu Pro Leu Gly Gly Ala His Lys Asp Ile 260 265 270
- Glu Gln Gln Ala Leu Ala Ile Lys Ser Ala Phe Val Ala Gln Leu Asp 275 280 285
- Ser Leu Glu Ser Leu Ser Arg Asp Glu Ile Ala Asn Asp Arg Phe Glu 290 295 300

Lys Phe Arg Asn Ile Gly Ser Tyr Ile Glu 305 310 <210> 75 <211> 945 <212> DNA <213> Staphylococcus aureus <400> 75 atgttagatt ttgaaaaacc actttttgaa attcgaaata aaattgaatc tttaaaagaa 60 tctcaagata aaaatgatgt ggatttacaa gaagaaattg acatgcttga agcgtcattg 120 gaacgagaaa ctaaaaaaat atatacaaat ctaaaaccat gggatcgtgt gcaaattgcg 180 cgtttgcaag aaagacctac gaccctagat tatattccat atatctttga ttcgtttatg 240 gaactacatg gtgatcgtaa ttttagagat gatccagtaa tgattggtgg tattggcttt 300 ttaaatggtc gtgctgttac agttattgga caacaacgtg gaaaagatac aaaagataat 360 atttatcgaa attttggtat ggcgcatcca gaaggttatc gaaaagcatt acgtttaatg 420 aaacaagctg aaaaattcaa tcgtcctatc tttacattta tagatacaaa aggtgcatat 480 cctggtaaag ctgctgaaga acgtggacaa agtgaatcta tcgcaacaaa tttgattgag 540 atggcttcat taaaagtacc agttattgcg attgtcattg gtgaaggtgg cagtggaggt 600 gctctaggta ttggtattgc caataaagta ttgatgttag agaatagtac ttactctgtt 660 atateteetg aaggtgeage ggeattatta tggaaagaca gtaatttgge taaaattgea 720 gctgaaacaa tgaaaattac tgcccatgat attaagcaat taggtattat agatgatgtc 780 atttctgaac cacttggcgg tgcacataaa gatattgaac agcaagcttt agctattaaa 840 tragegttig tigracagti agattracti gagtrattat cargigatga aattgriaat 900 gatcgctttg aaaaattcag aaatatcggt tcttatatag aataa <210> 76 <211> 314 <212> PRT <213> Staphylococcus aureus <400> 76 Met Leu Asp Phe Glu Lys Pro Leu Phe Glu Ile Arg Asn Lys Ile Glu Ser Leu Lys Glu Ser Gln Asp Lys Asn Asp Val Asp Leu Gln Glu Glu Ile Asp Met Leu Glu Ala Ser Leu Glu Arg Glu Thr Lys Lys Ile Tyr Thr Asn Leu Lys Pro Trp Asp Arg Val Gln Ile Ala Arg Leu Gln Glu Arg Pro Thr Thr Leu Asp Tyr Ile Pro Tyr Ile Phe Asp Ser Phe Met 65 70 Glu Leu His Gly Asp Arg Asn Phe Arg Asp Pro Val Met Ile Gly Gly Ile Gly Phe Leu Asn Gly Arg Ala Val Thr Val Ile Gly Gln Gln 100

Arg Gly Lys Asp Thr Lys Asp Asn Ile Tyr Arg Asn Phe Gly Met Ala

120

115

His Pro Glu Gly Tyr Arg Lys Ala Leu Arg Leu Met Lys Gln Ala Glu 130 135 140

Pro Gly Lys Ala Ala Glu Glu Arg Gly Gln Ser Glu Ser Ile Ala Thr 165 170 175

Asn Leu Ile Glu Met Ala Ser Leu Lys Val Pro Val Ile Ala Ile Val 180 185 190

Ile Gly Glu Gly Gly Ser Gly Gly Ala Leu Gly Ile Gly Ile Ala Asn 195 200 205

Lys Val Leu Met Leu Glu Asn Ser Thr Tyr Ser Val Ile Ser Pro Glu 210 215 220

Gly Ala Ala Ala Leu Leu Trp Lys Asp Ser Asn Leu Ala Lys Ile Ala 225 230 235 240

Ala Glu Thr Met Lys Ile Thr Ala His Asp Ile Lys Gln Leu Gly Ile 245 250 255

Ile Asp Asp Val Ile Ser Glu Pro Leu Gly Gly Ala His Lys Asp Ile 260 265 270

Glu Gln Gln Ala Leu Ala Ile Lys Ser Ala Phe Val Ala Gln Leu Asp 275 280 285

Ser Leu Glu Ser Leu Ser Arg Asp Glu Ile Ala Asn Asp Arg Phe Glu 290 295 300

Lys Phe Arg Asn Ile Gly Ser Tyr Ile Glu 305

<210> 77

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 77

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40

<210> 78

<211> 34

<212> DNA

<213> Artificial Sequence

<220×

<223> Description of Artificial Sequence: Synthetic
 primer

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<400> 78
gcgcggatcc accatgtagt tccataaacg aatc
                                                                    34
<210> 79
<211> 15
<212> PRT
<213> Staphylococcus aureus
<400> 79
Met Ala Ser Leu Lys Val Pro Val Ile Ala Ile Val Ile Gly Glu
<210> 80
<211> 20
<212> PRT
<213> Staphylococcus aureus
<400> 80
Gln Gln Ala Leu Ala Ile Lys Ser Ala Phe Val Ala Gln Leu Asp Ser
  1
Leu Glu Ser Leu
<210> 81
<211> 10
<212> PRT
<213> Staphylococcus aureus
<400> 81
Thr Leu Asp Tyr Ile Pro Tyr Ile Phe Asp
                      .
<210> 82
<211> 1356
<212> DNA
<213> Staphylococcus aureus
<400> 82
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gaattggcat ttaaattagg aagatacggt ggctatgttc tagcacataa taaaggtgaa 120
aaacacccac gtgtacttgt aggtcgcgat actagagttt caggtgaaat gttagaatca 180
gcattaatag ctggtttgat ttcaattggt gcagaagtga tgcgattagg tattatttca 240
acaccaggtg ttgcatattt aacacgcgat atgggtgcag agttaggtgt aatgatttca 300
gcctctcata atccagttgc agataatggt attaaattct ttggatcaga tggttttaaa 360
ctatcagatg aacaagaaaa tgaaattgaa gcattattgg atcaagaaaa cccagaatta 420
ccaagaccag ttggcaatga tattgtacat tattcagatt actttgaagg ggcacaaaaa 480
tatttgagct atttaaaatc aacagtagat gttaactttg aaggtttgaa aattgcttta 540
gatggtgcaa atggttcaac atcatcacta gcgccattct tatttggtga cttagaagca 600
gatactgaaa caattggatg tagtcctgat ggatataata tcaatgagaa atgtggctct 660
acacatcctg aaaaattagc tgaaaaagta gttgaaactg aaagtgattt tgggttagca 720
tttgacggcg atggagacag aatcatagca gtagatgaga atggtcaaat cgttgacggt 780
gaccaaatta tgtttattat tggtcaagaa atgcataaaa atcaagaatt gaataatgac 840
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atgattgttt ctactgttat gagtaattta ggtttttaca aagcgcttga acaagaagga 900 attaaatcta ataaaactaa agttggcgac agatatgtag tagaagaaat gcgtcgcggt 960

aattataact taggtggaga acaatctgga catatcgtta tgatggatta caatacaact 1020 ggtgatggtt tattaactgg tattcaatta gcttctgtaa taaaaatgac tggtaaatca 1080 ctaagtgaat tagctggaca aatgaaaaaa tatccacaat cattaattaa cgtacgcgta 1140 acagataaat atcgtgttga agaaaatgtt gacgttaaag aagttatgac taaagtagaa 1200 gtagaaatga atggagaagg tcgaatttta gtaagacctt ctggaacaga accattagtt 1260 cgtgtcatgg ttgaagcagc aactgatgaa gatgctgaaa gatttgcaca acaaatagct 1320 gatgtggttc aagataaaat gggattagat aaataa <210> 83 <211> 451 <212> PRT <213> Staphylococcus aureus <400> 83 Met Gly Lys Tyr Phe Gly Thr Asp Gly Val Arg Gly Val Ala Asn Gln Glu Leu Thr Pro Glu Leu Ala Phe Lys Leu Gly Arg Tyr Gly Gly Tyr Val Leu Ala His Asn Lys Gly Glu Lys His Pro Arg Val Leu Val Gly Arg Asp Thr Arg Val Ser Gly Glu Met Leu Glu Ser Ala Leu Ile Ala Gly Leu Ile Ser Ile Gly Ala Glu Val Met Arg Leu Gly Ile Ile Ser Thr Pro Gly Val Ala Tyr Leu Thr Arg Asp Met Gly Ala Glu Leu Gly Val Met Ile Ser Ala Ser His Asn Pro Val Ala Asp Asn Gly Ile Lys 105 Phe Phe Gly Ser Asp Gly Phe Lys Leu Ser Asp Glu Gln Glu Asn Glu Ile Glu Ala Leu Leu Asp Gln Glu Asn Pro Glu Leu Pro Arg Pro Val Gly Asn Asp Ile Val His Tyr Ser Asp Tyr Phe Glu Gly Ala Gln Lys 145 150 155 Tyr Leu Ser Tyr Leu Lys Ser Thr Val Asp Val Asn Phe Glu Gly Leu Lys Ile Ala Leu Asp Gly Ala Asn Gly Ser Thr Ser Ser Leu Ala Pro Phe Leu Phe Gly Asp Leu Glu Ala Asp Thr Glu Thr Ile Gly Cys Ser 200 Pro Asp Gly Tyr Asn Ile Asn Glu Lys Cys Gly Ser Thr His Pro Glu 210

Lys Leu Ala Glu Lys Val Val Glu Thr Glu Ser Asp Phe Gly Leu Ala 225 230 235 240

Phe Asp Gly Asp Gly Asp Ile Ile Ala Val Asp Glu Asn Gly Gln
245 250 255

Ile Val Asp Gly Asp Gln Ile Met Phe Ile Ile Gly Gln Glu Met His 260 265 270

Lys Asn Gln Glu Leu Asn Asn Asp Met Ile Val Ser Thr Val Met Ser 275 280 285

Asn Leu Gly Phe Tyr Lys Ala Leu Glu Glu Gly Ile Lys Ser Asn 290 295 300

Lys Thr Lys Val Gly Asp Arg Tyr Val Val Glu Glu Met Arg Arg Gly 305 310 315 320

Asn Tyr Asn Leu Gly Gly Glu Gln Ser Gly His Ile Val Met Met Asp 325 330 335

Tyr Asn Thr Thr Gly Asp Gly Leu Leu Thr Gly Ile Gln Leu Ala Ser 340 345 350

Val Ile Lys Met Thr Gly Lys Ser Leu Ser Glu Leu Ala Gly Gln Met 355 360 365

Lys Lys Tyr Pro Gln Ser Leu Ile Asn Val Arg Val Thr Asp Lys Tyr 370 380

Arg Val Glu Glu Asn Val Asp Val Lys Glu Val Met Thr Lys Val Glu 385 390 395 400

Val Glu Met Asn Gly Glu Gly Arg Ile Leu Val Arg Pro Ser Gly Thr 405 410 415

Glu Pro Leu Val Arg Val Met Val Glu Ala Ala Thr Asp Glu Asp Ala
420 425 430

Glu Arg Phe Ala Gln Gln Ile Ala Asp Val Val Gln Asp Lys Met Gly
435
440
445

Leu Asp Lys 450

<210> 84

<211> 1356

<212> DNA

<213> Staphylococcus aureus

<400> 84

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gcctctcata atccagttgc agataatggt attaaattct ttggatcaga tggttttaaa 360
ctatcagatg aacaagaaaa tgaaattgaa gcattattgg atcaagaaaa cccagaatta 420
ccaagaccag ttggcaatga tattgtacat tattcagatt actttgaagg ggcacaaaaa 480
tatttgagct atttaaaatc aacagtagat gttaactttg aaggtttgaa aattgcttta 540
gatggtgcaa atggttcaac atcatcacta gcgccattct tatttggtga cttagaagca 600
gatactgaaa caattggatg tagtcctgat ggatataata tcaatgagaa atgtggctct 660
acacatcctg aaaaattagc tgaaaaagta gttgaaactg aaagtgattt tgggttagca 720
tttgacggcg atggagacag aatcatagca gtagatgaga atggtcaaat cgttgacggt 780
gaccaaatta tgtttattat tggtcaagaa atgcataaaa atcaagaatt gaataatgac 840
atgattgttt ctactgttat gagtaattta ggtttttaca aagcgcttga acaagaagga 900
attaaatcta ataaaactaa agttggcgac agatatgtag tagaagaaat gcgtcgcggt 960
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ctaagtgaat tagctggaca aatgaaaaaa tatccacaat cattaattaa cgtacgcgta 1140
acagataaat atcgtgttga agaaaatgtt gacgttaaag aagttatgac taaagtagaa 1200
gtagaaatga atggagaagg tcgaatttta gtaagacctt ctggaacaga accattagtt 1260
cgtgtcatgg ttgaagcagc aactgatgaa gatgctgaaa gatttgcaca acaaatagct 1320
gatgtggttc aagataaaat gggattagat aaataa
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<210> 85
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<211> 451

<212> PRT

<213> Staphylococcus aureus

<400> 85

Met Gly Lys Tyr Phe Gly Thr Asp Gly Val Arg Gly Val Ala Asn Gln

1 10 15

Glu Leu Thr Pro Glu Leu Ala Phe Lys Leu Gly Arg Tyr Gly Gly Tyr 20 25 30

Val Leu Ala His Asn Lys Gly Glu Lys His Pro Arg Val Leu Val Gly 35 40 45

Arg Asp Thr Arg Val Ser Gly Glu Met Leu Glu Ser Ala Leu Ile Ala
50 55 60

Gly Leu Ile Ser Ile Gly Ala Glu Val Met Arg Leu Gly Ile Ile Ser 65 70 75 80

Thr Pro Gly Val Ala Tyr Leu Thr Arg Asp Met Gly Ala Glu Leu Gly 85 90 95

Val Met Ile Ser Ala Ser His Asn Pro Val Ala Asp Asn Gly Ile Lys 100 105 110

Phe Phe Gly Ser Asp Gly Phe Lys Leu Ser Asp Glu Gln Glu Asn Glu 115 120 125

Ile Glu Ala Leu Leu Asp Gln Glu Asn Pro Glu Leu Pro Arg Pro Val 130 135 140

Gly Asn Asp Ile Val His Tyr Ser Asp Tyr Phe Glu Gly Ala Gln Lys 145 150 155 160

Tyr Leu Ser Tyr Leu Lys Ser Thr Val Asp Val Asn Phe Glu Gly Leu 165 170 175 Lys Ile Ala Leu Asp Gly Ala Asn Gly Ser Thr Ser Ser Leu Ala Pro 180 185 190

Phe Leu Phe Gly Asp Leu Glu Ala Asp Thr Glu Thr Ile Gly Cys Ser 195 200 205

Pro Asp Gly Tyr Asn Ile Asn Glu Lys Cys Gly Ser Thr His Pro Glu 210 215 220

Lys Leu Ala Glu Lys Val Val Glu Thr Glu Ser Asp Phe Gly Leu Ala 225 230 235 240

Phe Asp Gly Asp Gly Asp Ile Ile Ala Val Asp Glu Asn Gly Gln
245 250 255

Ile Val Asp Gly Asp Gln Ile Met Phe Ile Ile Gly Gln Glu Met His 260 265 270

Lys Asn Gln Glu Leu Asn Asn Asp Met Ile Val Ser Thr Val Met Ser 275 280 285

Asn Leu Gly Phe Tyr Lys Ala Leu Glu Glu Gly Ile Lys Ser Asn 290 295 300

Lys Thr Lys Val Gly Asp Arg Tyr Val Val Glu Glu Met Arg Arg Gly 305 310 315 320

Asn Tyr Asn Leu Gly Gly Glu Gln Ser Gly His Ile Val Met Met Asp 325 330 335

Tyr Asn Thr Thr Gly Asp Gly Leu Leu Thr Gly Ile Gln Leu Ala Ser 340 345 350

Val Ile Lys Met Thr Gly Lys Ser Leu Ser Glu Leu Ala Gly Gln Met 355 360 365

Lys Lys Tyr Pro Gln Ser Leu Ile Asn Val Arg Val Thr Asp Lys Tyr 370 375 380

Arg Val Glu Glu Asn Val Asp Val Lys Glu Val Met Thr Lys Val Glu 385 390 395 400

Val Glu Met Asn Gly Glu Gly Arg Ile Leu Val Arg Pro Ser Gly Thr 405 410 415

Glu Pro Leu Val Arg Val Met Val Glu Ala Ala Thr Asp Glu Asp Ala 420 425 430

Glu Arg Phe Ala Gln Gln Ile Ala Asp Val Val Gln Asp Lys Met Gly
435 440 445

Leu Asp Lys 450

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<210> 86
<211> 34
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
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<400> 86
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                                                                    34
<210> 87
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 87
gcgcggatcc aacacctggt gttgaaataa tac
                                                                    33
<210> 88
<211> 10
<212> PRT
<213> Staphylococcus aureus
<400> 88
Thr Glu Pro Leu Val Arg Val Met Val Glu
                 5
<210> 89
<211> 12
<212> PRT
<213> Staphylococcus aureus
<400> 89
Leu Thr Gly Ile Gln Leu Ala Ser Val Ile Lys Met
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<210> 90
<211> 9
<212> PRT
<213> Staphylococcus aureus
His Pro Arg Val Leu Val Gly Arg Asp
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<210> 91

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<211> 1044
 <212> DNA
 <213> Streptococcus pneumoniae
<400> 91
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tttatcagtc agtcaggtga ctttatcaaa acacaggaat ttagtcatgc tccggggcaa 180
gaagaccgtc tcatgaccaa tgaaaccatt gattgggata agaaagttgc accaagtgct 240
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tctgttcaag gattcttgga agttttgaaa atgccttacg ttggttgcaa cattttgtca 360
tcaagtcttg ccatggataa aatcacgact aagcgtgttc tggaatctgc tggtattgcc 420
caagtteett atgtggetat egttgaagge gatgatgtga etgetaaaat egetgaagtg 480
gaagaaaaat tggcttatcc agtcttcact aagccgtcaa acatggggtc tagtgtcggt 540
atttctaagt ctgaaaacca agaagaactc cgtcaagcct taaaacttgc cttccgatat 600
gacagccgtg tcttggttga gcaaggagtg aatgcccgtg aaattgaggt tggcctcttg 660
ggtaactacg atgtcaagag cacgctacca ggagaagttg tcaaggacgt tgccttttat 720
gactacgatg ccaagtatat tgataacaat attactatgg atattcctgc caaaatcagt 780
gatgatgtgg tggctgtcat gcgtcaaaat gcagaaacag ccttccgtgc cattggtggc 840
cttggtctat ctcgttgcga tttcttctat acagataagg gagagatttt tctcaacgag 900
ctcaatacta tgccaggttt cacccagtgg tctatgtacc cactactttg ggacaatatg 960
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aagcgcgaag cgcatttgat ataa
<210> 92
<211> 347
<212> PRT
<213> Streptococcus pneumoniae
<400> 92
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Glu Val Ser Val Leu Ser Ala Glu Ser Val Met Arg Ala Val Asp Tyr
Asp Arg Phe Thr Val Lys Thr Phe Phe Ile Ser Gln Ser Gly Asp Phe
Ile Lys Thr Gln Glu Phe Ser His Ala Pro Gly Gln Glu Asp Arg Leu
Met Thr Asn Glu Thr Ile Asp Trp Asp Lys Lys Val Ala Pro Ser Ala
                     70
Ile Tyr Glu Glu Gly Ala Val Val Phe Pro Val Leu His Gly Pro Met
Gly Glu Asp Gly Ser Val Gln Gly Phe Leu Glu Val Leu Lys Met Pro
Tyr Val Gly Cys Asn Ile Leu Ser Ser Ser Leu Ala Met Asp Lys Ile
Thr Thr Lys Arg Val Leu Glu Ser Ala Gly Ile Ala Gln Val Pro Tyr
                        135
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Val Ala Ile Val Glu Gly Asp Asp Val Thr Ala Lys Ile Ala Glu Val Glu Glu Lys Leu Ala Tyr Pro Val Phe Thr Lys Pro Ser Asn Met Gly 165 170 Ser Ser Val Gly Ile Ser Lys Ser Glu Asn Gln Glu Leu Arg Gln 185 Ala Leu Lys Leu Ala Phe Arg Tyr Asp Ser Arg Val Leu Val Glu Gln 200 Gly Val Asn Ala Arg Glu Ile Glu Val Gly Leu Leu Gly Asn Tyr Asp Val Lys Ser Thr Leu Pro Gly Glu Val Val Lys Asp Val Ala Phe Tyr 230 Asp Tyr Asp Ala Lys Tyr Ile Asp Asn Asn Ile Thr Met Asp Ile Pro 250 Ala Lys Ile Ser Asp Asp Val Val Ala Val Met Arg Gln Asn Ala Glu Thr Ala Phe Arg Ala Ile Gly Gly Leu Gly Leu Ser Arg Cys Asp Phe 280 285 Phe Tyr Thr Asp Lys Gly Glu Ile Phe Leu Asn Glu Leu Asn Thr Met Pro Gly Phe Thr Gln Trp Ser Met Tyr Pro Leu Leu Trp Asp Asn Met 310 Gly Ile Ser Tyr Pro Lys Leu Ile Glu Arg Leu Val Asp Leu Ala Lys 325 330 Glu Ser Phe Asp Lys Arg Glu Ala His Leu Ile <210> 93

<211> 1044

<212> DNA

<213> Streptococcus pneumoniae

<400> 93

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ggtaactacg atgtcaagag cacgctacct ggagaagttg tcaaggacgt tgccttttat 720 gactacgatg ccaagtatat tgataacaag attactatgg atattcctac caaaatcagt 780 gatgatgtgg tggctgtcat gcgtcaaaat gcagaaacag ccttccgtgc cattggtggc 840 cttggtctat ctcgttgcga tttcttctat acagataagg gagagatttt tctcaacgag 900 ctcaatacca tgccaggttt cacccagtgg tctatgtacc cactactttg ggacaatatg 960 gggatcagct acccagaact aatcgagcgt ttggttgacc ttgccaagga aagttttgac 1020 aagcgcgaag cgcatttgat ataa

<210> 94

<211> 347

<212> PRT

<213> Streptococcus pneumoniae

<400> 94

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Asp Arg Phe Thr Val Lys Thr Phe Phe Ile Ser Gln Ser Gly Asp Phe 35 40 45

Ile Lys Thr Gln Glu Phe Ser His Ala Pro Gly Gln Glu Asp Arg Leu 50 55 60

Met Thr Asn Glu Thr Ile Asp Trp Asp Lys Lys Val Ala Pro Ser Ala 65 70 75 80

Ile Tyr Glu Glu Gly Ala Val Val Phe Pro Val Leu His Gly Pro Met
, 85 90 95

Gly Glu Asp Gly Ser Val Gln Gly Phe Leu Glu Val Leu Lys Met Pro 100 105 110

Tyr Val Gly Cys Asn Ile Leu Ser Ser Ser Leu Ala Met Asp Lys Ile 115 120 125

Thr Thr Lys Arg Val Leu Glu Ser Ala Gly Ile Ala Gln Val Pro Tyr 130 135 140

Val Ala Ile Val Glu Gly Asp Asp Val Thr Ala Lys Ile Ala Glu Val 145 150 155 160

Glu Glu Lys Leu Ala Tyr Pro Val Phe Ile Lys Pro Ser Asn Met Gly
165 170

Ser Ser Val Gly Ile Ser Lys Ser Glu Asn Gln Glu Glu Leu Arg Gln 180 185 190

Ala Leu Lys Leu Ala Phe Arg Tyr Asp Ser Arg Val Leu Val Glu Gln
195 200 205

Gly Val Asn Ala Arg Glu Ile Glu Val Gly Leu Leu Gly Asn Tyr Asp 210 215 220

Val Lys Ser Thr Leu Pro Gly Glu Val Val Lys Asp Val Ala Phe Tyr Asp Tyr Asp Ala Lys Tyr Ile Asp Asn Lys Ile Thr Met Asp Ile Pro 250 Thr Lys Ile Ser Asp Asp Val Val Ala Val Met Arg Gln Asn Ala Glu Thr Ala Phe Arg Ala Ile Gly Gly Leu Gly Leu Ser Arg Cys Asp Phe 280 Phe Tyr Thr Asp Lys Gly Glu Ile Phe Leu Asn Glu Leu Asn Thr Met 290 Pro Gly Phe Thr Gln Trp Ser Met Tyr Pro Leu Leu Trp Asp Asn Met 310 315 Gly Ile Ser Tyr Pro Glu Leu Ile Glu Arg Leu Val Asp Leu Ala Lys Glu Ser Phe Asp Lys Arg Glu Ala His Leu Ile 340 <210> 95 <211> 40 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic primer gcggcggccc atatgaaaca aacgattatt cttttatatg 40 <210> 96 <211> 29 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic primer <400> 96 gcgcggatcc tatcaaatgc gcttcgcgc 29 <210> 97 <211> 12 <212> PRT <213> Streptococcus pneumoniae

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<213> Streptococcus pneumoniae
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Ala Ile Val Glu Gly Asp
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<211> 9
<212> PRT
<213> Streptococcus pneumoniae
<400> 99
Asp Ser Arg Val Leu Val Glu Gln Gly
<210> 100
<211> 1353
<212> DNA
<213> Streptococcus pneumoniae
<400> 100
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gaattagcct ttaaactagg acgttttgga ggctatgttc ttagtcaaca tgaaacggaa 120
gcgccgaaag tctttgtagg acgtgacaca cgtatttcag gggaaatgtt ggaatcggcc 180
ttggtggcag gtctcctttc agtagggatt cacgtataca aacttggtgt ccttgcaaca 240
ccagcagtag cttacttggt tgaaactgaa ggagcaagtg ccggtgtcat gatttctgct 300
agccacaacc cagcccttga taacggaatc aagttctttg gcggtgatgg cttcaaacta 360
gatgatgaaa aagaagcaga aattgaagcc ttgctagatg ctgaggaaga cactcttcct 420
cgtccaagtg cagaaggctt aggaattttg gtagattatc cagaaggctt gcgtaagtat 480
gaaggatacc ttgtttcaac tggaactcct cttgatggaa tgaaggttgc cttggataca 540
gctaatggag cagcttctac cagtgcccgt caaatctttg cagaccttgg tgcccaattg 600
acggttatcg gggaaacacc agacggtctt aacatcaacc ttaatgttgg ttcaacacat 660
ccagaagccc ttcaagaagt ggtcaaagaa agtgggtcag ctattggttt ggcctttgat 720
ggagacagtg accgcttgat tgctgttgat gagaatggtg acatcgttga tggtgacaag 780
attatgtaca tcatcggaaa atacctttct gaaaaaggac aattggctca aaatacaatt 840
gtgacaactg ttatgtctaa ccttggtttc cacaaggcct tgaatcgcga aggtattaac 900
aaggcagtta ctgcagttgg tgaccgctac gttgttgaag aaatgagaaa atcaggctac 960
aaccttggtg gtgaacagtc tggtcacgtt atcttgatgg attacaatac cacaggtgat 1020
ggtcaattat cagcagttca attgactaaa atcatgaagg aaactggtaa gagcttatca 1080
gagttggcgg cagaagtaac gatttatcca caaaaattag ttaatatccg agtggaaaac 1140
gtcatgaagg aaaaggccat ggaagtgcca gctatcaagg ccatcatcga gaagatggaa 1200
gaagaaatgg cggggaacgg ccgtatcctt gttcgtccaa gtggaacaga acccctcttg 1260
cgtgttatgg cagaagcgcc tacaacagaa gaagtaaact actatgttga taccatcaca 1320
gatgtagttc gtgctgaaat tgggattgac taa
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- <210> 101
- <211> 450
- <212> PRT
- <213> Streptococcus pneumoniae
- <400> 101
- Met Gly Lys Tyr Phe Gly Thr Asp Gly Val Arg Gly Glu Ala Asn Leu

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- Glu Leu Thr Pro Glu Leu Ala Phe Lys Leu Gly Arg Phe Gly Gly Tyr 20 25 30
- Val Leu Ser Gln His Glu Thr Glu Ala Pro Lys Val Phe Val Gly Arg 35 40 45
- Asp Thr Arg Ile Ser Gly Glu Met Leu Glu Ser Ala Leu Val Ala Gly
 50 55 60
- Leu Leu Ser Val Gly Ile His Val Tyr Lys Leu Gly Val Leu Ala Thr 65 70 75 80
- Pro Ala Val Ala Tyr Leu Val Glu Thr Glu Gly Ala Ser Ala Gly Val
- Met Ile Ser Ala Ser His Asn Pro Ala Leu Asp Asn Gly Ile Lys Phe 100 105 110
- Phe Gly Gly Asp Gly Phe Lys Leu Asp Asp Glu Lys Glu Ala Glu Ile 115 120 125
- Glu Ala Leu Leu Asp Ala Glu Glu Asp Thr Leu Pro Arg Pro Ser Ala 130 135 140
- Glu Gly Leu Gly Ile Leu Val Asp Tyr Pro Glu Gly Leu Arg Lys Tyr 145 150 155 160
- Glu Gly Tyr Leu Val Ser Thr Gly Thr Pro Leu Asp Gly Met Lys Val 165 170 175
- Ala Leu Asp Thr Ala Asn Gly Ala Ala Ser Thr Ser Ala Arg Gln Ile 180 185 190
- Phe Ala Asp Leu Gly Ala Gln Leu Thr Val Ile Gly Glu Thr Pro Asp 195 200 205
- Gly Leu Asn Ile Asn Leu Asn Val Gly Ser Thr His Pro Glu Ala Leu 210 215 220
- Gln Glu Val Val Lys Glu Ser Gly Ser Ala Ile Gly Leu Ala Phe Asp 225 230 235 240
- Gly Asp Ser Asp Arg Leu Ile Ala Val Asp Glu Asn Gly Asp Ile Val 245 250 255
- Asp Gly Asp Lys Ile Met Tyr Ile Ile Gly Lys Tyr Leu Ser Glu Lys 260 265 270

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Gly Gln Leu Ala Gln Asn Thr Ile Val Thr Thr Val Met Ser Asn Leu
                            280
Gly Phe His Lys Ala Leu Asn Arg Glu Gly Ile Asn Lys Ala Val Thr
Ala Val Gly Asp Arg Tyr Val Val Glu Glu Met Arg Lys Ser Gly Tyr
305
                    310
                                         315
Asn Leu Gly Gly Glu Gln Ser Gly His Val Ile Leu Met Asp Tyr Asn
                                     330
Thr Thr Gly Asp Gly Gln Leu Ser Ala Val Gln Leu Thr Lys Ile Met
Lys Glu Thr Gly Lys Ser Leu Ser Glu Leu Ala Ala Glu Val Thr Ile
                            360
Tyr Pro Gln Lys Leu Val Asn Ile Arg Val Glu Asn Val Met Lys Glu
Lys Ala Met Glu Val Pro Ala Ile Lys Ala Ile Ile Glu Lys Met Glu
385
                                         395
Glu Glu Met Ala Gly Asn Gly Arg Ile Leu Val Arg Pro Ser Gly Thr
Glu Pro Leu Leu Arg Val Met Ala Glu Ala Pro Thr Thr Glu Glu Val
                                425
Asn Tyr Tyr Val Asp Thr Ile Thr Asp Val Val Arg Ala Glu Ile Gly
                            440
Ile Asp
    450
<210> 102
<211> 1353
<212> DNA
<213> Streptococcus pneumoniae
<400> 102
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gcgccgaaag tctttgtagg acgtgacaca cgtatttcag gggaaatgct ggaatcggcc 180
ttggtggcag gtctcctttc agtagggatt cacgtataca aacttggtgt ccttgcaaca 240
tragcagtag cttacttggt tgaaactgaa ggagcaagtg ccggtgtcat gatttctgct 300
agccacaacc cagccettga taacggaatc aagttetttg geggtgatgg etteaaacta 360
gatgatgaaa aagaagcaga aattgaagcc ttgctagatg ctgaggaaga cactcttcct 420
cggccaagtg cagaaggttt aggaatcttg gtagattatc cagaaggctt gcgtaagtat 480
gaaggatacc ttgtttcaac tggaactcct cttgatggaa tgaaggttgc cttggataca 540
gctaatggag cagcttctac cagtgcccgt caaatctttg cagaccttgg tgcccaattg 600
acggttatcg gggaaacacc agacggtctt aacatcaacc ttaatgttgg ttcaacacat 660
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ccagaagcc ttcaagaagt ggtcaaagaa agtgggtcag ctattggttt ggcctttgat 720 ggagacagtg accgcttgat tgctgttgat gagaatggtg acatcgttga tggtgacaag 780 attatgtaca tcatcggaaa atacctttct gaaaaaggac aattggctca aaatacaatt 840 gtgacaactg ttatgtctaa ccttggtttc cacaaggcct tgaatcgcga aggtattaac 900

aaggcagtta ctgcagttgg tgaccgctac gttgttgaag aaatgagaaa atcaggctac 960 aaccttggtg gtgaacagtc tggtcacgtt atcttgatgg attacaatac cacaggtgat 1020 ggtcaattat cagcagttca attgactaaa atcatgaagg aaactggtaa gagcttatca 1080 gagttggcgg cagaagtaac gatttatcca caaaaattag ttaatatccg agtggaaaac 1140 gtcatgaagg aaaaggccat ggaagtgcca gctatcaagg ccatcatcga gaagatggaa 1200 gaagaaatgg cggggaacgg ccgtatcctt gttcgtccaa gtggaacaga acccctcttg 1260 cgtgttatgg cagaaggcc tacaacagaa gaagtaaact actatgttga taccatcaca 1320 gatgtagttc gtgctgaaat tgggattgac taa 1353

<210> 103

<211> 450

<212> PRT

<213> Streptococcus pneumoniae

<400> 103

Met Gly Lys Tyr Phe Gly Thr Asp Gly Val Arg Gly Glu Ala Asn Leu

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20 25 30

Val Leu Ser Gln His Glu Thr Glu Ala Pro Lys Val Phe Val Gly Arg 35 40 45

Asp Thr Arg Ile Ser Gly Glu Met Leu Glu Ser Ala Leu Val Ala Gly 50 55 60

Leu Leu Ser Val Gly Ile His Val Tyr Lys Leu Gly Val Leu Ala Thr 65 70 75 80

Ser Ala Val Ala Tyr Leu Val Glu Thr Glu Gly Ala Ser Ala Gly Val 85 90 95

Met Ile Ser Ala Ser His Asn Pro Ala Leu Asp Asn Gly Ile Lys Phe 100 105 110

Phe Gly Gly Asp Gly Phe Lys Leu Asp Asp Glu Lys Glu Ala Glu Ile 115 120 125

Glu Ala Leu Leu Asp Ala Glu Glu Asp Thr Leu Pro Arg Pro Ser Ala 130 135 140

Glu Gly Leu Gly Ile Leu Val Asp Tyr Pro Glu Gly Leu Arg Lys Tyr 145 150 155 160

Glu Gly Tyr Leu Val Ser Thr Gly Thr Pro Leu Asp Gly Met Lys Val 165 170 175

Ala Leu Asp Thr Ala Asn Gly Ala Ala Ser Thr Ser Ala Arg Gln Ile 180 185 190

Phe Ala Asp Leu Gly Ala Gln Leu Thr Val Ile Gly Glu Thr Pro Asp 195 200 205

Gly Leu Asn Ile Asn Leu Asn Val Gly Ser Thr His Pro Glu Ala Leu 210 215 220 Gln Glu Val Val Lys Glu Ser Gly Ser Ala Ile Gly Leu Ala Phe Asp 225 230 235 240

Gly Asp Ser Asp Arg Leu Ile Ala Val Asp Glu Asn Gly Asp Ile Val 245 250 255

Asp Gly Asp Lys Ile Met Tyr Ile Ile Gly Lys Tyr Leu Ser Glu Lys 260 265 270

Gly Gln Leu Ala Gln Asn Thr Ile Val Thr Thr Val Met Ser Asn Leu 275 280 285

Gly Phe His Lys Ala Leu Asn Arg Glu Gly Ile Asn Lys Ala Val Thr 290 295 300

Ala Val Gly Asp Arg Tyr Val Val Glu Glu Met Arg Lys Ser Gly Tyr 305 310 315 320

Asn Leu Gly Gly Glu Gln Ser Gly His Val Ile Leu Met Asp Tyr Asn 325 330 335

Thr Thr Gly Asp Gly Gln Leu Ser Ala Val Gln Leu Thr Lys Ile Met 340 345 350

Lys Glu Thr Gly Lys Ser Leu Ser Glu Leu Ala Ala Glu Val Thr Ile 355 360 365

Tyr Pro Gln Lys Leu Val Asn Ile Arg Val Glu Asn Val Met Lys Glu 370 375 380

Lys Ala Met Glu Val Pro Ala Ile Lys Ala Ile Ile Glu Lys Met Glu 385 390 395 400

Glu Glu Met Ala Gly Asn Gly Arg Ile Leu Val Arg Pro Ser Gly Thr 405 410 415

Glu Pro Leu Leu Arg Val Met Ala Glu Ala Pro Thr Thr Glu Glu Val 420 425 430

Asn Tyr Tyr Val Asp Thr Ile Thr Asp Val Val Arg Ala Glu Ile Gly
435 440 445

Ile Asp 450

<210> 104

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 104

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 <210> 106
 <211> 34
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Synthetic
       primer
 <400> 106
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<210> 107
<211> 33
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
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<400> 107
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<210> 108
<211> 31
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic
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<400> 108
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<210> 109
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<213> Artificial Sequence
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<210> 110
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<212> DNA
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      primer
<400> 110
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                                                                    31
<210> 111
<211> 32
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic
      primer
<400> 111
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                                                                    32
<210> 112
<211> 31
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<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic
      primer
<400> 112
gcgcggatcc tacatctgtg atggtatcaa c
                                                                    31
<210> 113
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 113
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 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Synthetic
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<210> 115
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
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<400> 115
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                                                                   31
<210> 116
<211> 32
<212> PRT
<213> Streptococcus pneumoniae
<400> 116
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Lys Leu Gly Val Leu Ala Thr Pro Ala Val Ala Tyr Leu Val Glu Thr
<210> 117
<211> 8
<212> PRT
<213> Streptococcus pneumoniae
<400> 117
Leu Ser Ala Val Gln Leu Thr Lys
            5
<210> 118
<211> 22
<212> PRT
<213> Streptococcus pneumoniae
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 Asn Ile Arg Val Glu Asn
             20
 <210> 119
 <211> 1353
 <212> DNA
 <213> Streptococcus pneumoniae
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aaacctttcg aggacaatcc agctgcccaa agtttgctgg aagaagggat caaggtcatt 180
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ggtcttttat cagggaatat cggctatcca gctagtcagg ttgctcaaat agcatcagat 480
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ccagagattg cggttattac caacctcatg ccaactcata tcgactacca tgggtcattt 600
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gagtttgacg aattggtgcc agacattact ggactcaaga agatggtcat cctgggtcaa 1140
tctgcagaac gtgtcaaacg ggcagcagac aaggctggtg tcgcttatgt ggaggcgaca 1200
gatattgcag atgcgacccg caaggcctat gagcttgcga ctcaaggaga tgtggttctt 1260
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<210> 120
<211> 450
<212> PRT
<213> Streptococcus pneumoniae
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Leu Ala Lys Ser Gly Glu Ser Ala Ala Arg Leu Leu Asp Lys Leu Gly
Ala Ile Val Thr Val Asn Asp Gly Lys Pro Phe Glu Asp Asn Pro Ala
Ala Gln Ser Leu Leu Glu Glu Gly Ile Lys Val Ile Thr Gly Gly His
    50
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- Pro Leu Glu Leu Leu Asp Glu Glu Phe Ala Leu Met Val Lys Asn Pro 65 70 75 80
- Gly Ile Pro Tyr Asn Asn Pro Met Ile Glu Lys Ala Leu Ala Lys Gly 85 90 95
- Ile Pro Val Leu Thr Glu Val Glu Leu Ala Tyr Leu Ile Ser Glu Ala
 100 105 110
- Pro Ile Ile Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Thr 115 120 125
- Met Ile Gly Glu Val Leu Thr Ala Ala Gly Gln His Gly Leu Leu Ser 130 140
- Lys Asp Thr Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met Gly Val
 165 170 175
- Gln Glu Phe His Pro Glu Ile Ala Val Ile Thr Asn Leu Met Pro Thr 180 185 190
- His Ile Asp Tyr His Gly Ser Phe Ser Glu Tyr Val Ala Ala Lys Trp 195 200 205
- Asn Ile Gln Asn Lys Met Thr Ala Ala Asp Phe Leu Val Leu Asn Phe 210 215 220
- Asn Gln Asp Leu Ala Lys Asp Leu Thr Ser Lys Thr Glu Ala Thr Val 225 230 235 240
- Val Pro Phe Ser Thr Leu Glu Lys Val Asp Gly Ala Tyr Leu Glu Asp 245 250 255
- Gly Gln Leu Tyr Phe Arg Gly Glu Val Val Met Ala Ala Asn Glu Ile 260 265 270
- Gly Val Pro Gly Ser His Asn Val Glu Asn Ala Leu Ala Thr Ile Ala 275 280 285
- Val Ala Lys Leu Arg Asp Val Asp Asn Gln Thr Ile Lys Glu Thr Leu 290 295 300
- Ser Ala Phe Gly Gly Val Lys His Arg Leu Gln Phe Val Asp Asp Ile 305 310 315 320
- Lys Gly Val Lys Phe Tyr Asn Asp Ser Lys Ser Thr Asn Ile Leu Ala 325 330 335
- Thr Gln Lys Ala Leu Ser Gly Phe Asp Asn Ser Lys Val Val Leu Ile 340 345 350
- Ala Gly Gly Leu Asp Arg Gly Asn Glu Phe Asp Glu Leu Val Pro Asp 355 360 365

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Ile Thr Gly Leu Lys Lys Met Val Ile Leu Gly Gln Ser Ala Glu Arg
    370
                       375
Val Lys Arg Ala Ala Asp Lys Ala Gly Val Ala Tyr Val Glu Ala Thr
Asp Ile Ala Asp Ala Thr Arg Lys Ala Tyr Glu Leu Ala Thr Gln Gly
                                   410
Asp Val Val Leu Leu Ser Pro Ala Asn Ala Ser Trp Asp Met Tyr Ala
                               425
Asn Phe Glu Val Arg Gly Asp Leu Phe Ile Asp Thr Val Ala Glu Leu
                           440
                                               445
Lys Glu
    450
<210> 121
<211> 1353
<212> DNA
<213> Streptococcus pneumoniae
<400> 121
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aagcettteg aggacaatee agetgeecaa agtttgetgg aagaagggat caaggteatt 180
acaggtggcc atcctttgga actcttggat gaagagtttg cccttatggt gaaaaatcca 240
ggtatcccct acaacaatcc catgattgaa aaggctttgg ccaagggaat tccaqtcttq 300
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gatattgcag atgcgacccg caaggcatat gagcttgcga ctcaaggaga tgtggttctt 1260
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<213> Streptococcus pneumoniae
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- Ala Ile Val Thr Val Asn Asp Gly Lys Pro Phe Glu Asp Asn Pro Ala 35 40 45
- Ala Gln Ser Leu Leu Glu Glu Gly Ile Lys Val Ile Thr Gly Gly His 50 55 60
- Pro Leu Glu Leu Leu Asp Glu Glu Phe Ala Leu Met Val Lys Asn Pro 65 70 75 80
- Gly Ile Pro Tyr Asn Asn Pro Met Ile Glu Lys Ala Leu Ala Lys Gly 85 90 95
- Ile Pro Val Leu Thr Glu Val Glu Leu Ala Tyr Leu Ile Ser Glu Ala 100 105 110
- Pro Ile Ile Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Thr 115 120 125
- Met Ile Gly Glu Val Leu Thr Ala Ala Gly Gln His Gly Leu Leu Ser 130 140
- Gly Asn Ile Gly Tyr Pro Ala Ser Gln Val Ala Gln Ile Ala Ser Asp 145 150 155 160
- Lys Asp Thr Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met Gly Val 165 170 175
- Gln Glu Phe His Pro Glu Ile Ala Val Ile Thr Asn Leu Met Pro Thr 180 185 190
- His Ile Asp Tyr His Gly Ser Phe Ser Glu Tyr Val Ala Ala Lys Trp 195 200 205
- Asn Ile Gln Asn Lys Met Thr Ala Ala Asp Phe Leu Val Leu Asn Phe 210 215 220
- Asn Gln Asp Leu Ala Lys Asp Leu Thr Ser Lys Thr Glu Ala Thr Val 225 230 235 240
- Val Pro Phe Ser Thr Leu Glu Lys Val Asp Gly Ala Tyr Leu Glu Asp 245 250 255
- Gly Gln Leu Tyr Phe Arg Gly Glu Val Val Met Ala Ala Asn Glu Ile 260 265 270
- Gly Val Pro Gly Ser His Asn Val Glu Asn Ala Leu Ala Thr Ile Ala 275 280 285
- Val Ala Lys Leu Arg Gly Val Asp Asn Gln Thr Ile Lys Glu Thr Leu 290 295 300
- Ser Ala Phe Gly Gly Val Lys His Arg Leu Gln Phe Val Asp Asp Ile 305 310 315 320

Lys Gly Val Lys Phe Tyr Asn Asp Ser Lys Ser Thr Asn Ile Leu Ala 330 Thr Gln Lys Ala Leu Ser Gly Phe Asp Asn Ser Lys Val Val Leu Ile Ala Gly Gly Leu Asp Arg Gly Asn Glu Phe Asp Glu Leu Val Pro Asp 360 Ile Thr Gly Leu Lys Lys Met Val Ile Leu Gly Gln Ser Ala Glu Arg Val Lys Arg Ala Ala Asp Lys Ala Gly Val Ala Tyr Val Glu Ala Thr Asp Ile Ala Asp Ala Thr Arg Lys Ala Tyr Glu Leu Ala Thr Gln Gly Asp Val Val Leu Leu Ser Pro Ala Asn Ala Ser Trp Asp Met Tyr Ala 425 Asn Phe Glu Val Arg Gly Asp Leu Phe Ile Asp Thr Val Ala Glu Leu Lys Glu 450 <210> 123 <211> 42 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic primer <400> 123 42 gcggcggccc atatgaaagt aatagatcaa tttaaaaata ag <210> 124 <211> 32 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Synthetic primer <400> 124 gcgcggatcc ttcttttaac tccgctactg tg 32 <210> 125 <211> 36 <212> DNA <213> Artificial Sequence

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<400> 136
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<213> Staphylococcus aureus
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ggatatgatg ttcgctattt gactggaacg gatgaacacg gtcaaaaaat tcaagaaaaa 180
gctcaaaaag ctggtaagac agaaattgaa tatttggatg agatgattgc tggaattaaa 240
caattgtggg ctaagcttga aatttcaaat gatgatttta tcagaacaac tgaagaacgt 300
cataaacatg tcgttgagca agtgtttgaa cgtttattaa agcaaggtga tatctattta 360
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gtagacccac aatacgaaaa cggtaaaatt attggtggca aaagtccaga ttctggacac 480
gaagttgaac tagttaaaga agaaagttat ttctttaata ttagtaaata tacagaccgt 540
ttattagagt tctatgacca aaatccagat tttatacaac caccatcaag aaaaaatgaa 600
atgattaaca acttcattaa accaggactt gctgatttag ctgtttctcg tacatcattt 660
aactggggtg tecatgttee gtetaateea aaacatgttg tttatgtttg gattgatgeg 720
ttagttaact atatttcagc attaggctat ttatcagatg atgagtcact atttaacaaa 780
tactggccag cagatattca tttaatggct aaggaaattg tgcgattcca ctcaattatt 840
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gctttagaaa cagtgaaaag ctacactgaa agcatggaaa gtttgcaatt ttctgtggca 1260
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<211> 657
<212> PRT
<213> Staphylococcus aureus
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Ile Ala Arg Tyr Lys Arg Met Gln Gly Tyr Asp Val Arg Tyr Leu Thr
                             40
Gly Thr Asp Glu His Gly Gln Lys Ile Gln Glu Lys Ala Gln Lys Ala
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- Gly Lys Thr Glu Ile Glu Tyr Leu Asp Glu Met Ile Ala Gly Ile Lys
 65 70 75 80

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- Gin Leu Trp Ala Lys Leu Glu Ile Ser Asn Asp Asp Phe Ile Arg Thr
 85 90 95
- Thr Glu Glu Arg His Lys His Val Val Glu Gln Val Phe Glu Arg Leu
 100 105 110
- Leu Lys Gln Gly Asp Ile Tyr Leu Gly Glu Tyr Glu Gly Trp Tyr Ser 115 120 125
- Val Pro Asp Glu Thr Tyr Tyr Thr Glu Ser Gln Leu Val Asp Pro Gln 130 135 140
- Tyr Glu Asn Gly Lys Ile Ile Gly Gly Lys Ser Pro Asp Ser Gly His 145 150 155 160
- Glu Val Glu Leu Val Lys Glu Glu Ser Tyr Phe Phe Asn Ile Ser Lys 165 170 175
- Tyr Thr Asp Arg Leu Leu Glu Phe Tyr Asp Gln Asn Pro Asp Phe Ile 180 185 190
- Gln Pro Pro Ser Arg Lys Asn Glu Met Ile Asn Asn Phe Ile Lys Pro 195 200 205
- Gly Leu Ala Asp Leu Ala Val Ser Arg Thr Ser Phe Asn Trp Gly Val 210 215 220
- His Val Pro Ser Asn Pro Lys His Val Val Tyr Val Trp Ile Asp Ala 225 230 235 240
- Leu Val Asn Tyr Ile Ser Ala Leu Gly Tyr Leu Ser Asp Asp Glu Ser 245 250 255
- Leu Phe Asn Lys Tyr Trp Pro Ala Asp Ile His Leu Met Ala Lys Glu 260 265 270
- Ile Val Arg Phe His Ser Ile Ile Trp Pro Ile Leu Leu Met Ala Leu 275 280 285
- Asp Leu Pro Leu Pro Lys Lys Val Phe Ala His Gly Trp Ile Leu Met 290 295 300
- Lys Asp Gly Lys Met Ser Lys Ser Lys Gly Asn Val Val Asp Pro Asn 305 310 315 320
- Ile Leu Ile Asp Arg Tyr Gly Leu Asp Ala Thr Arg Tyr Tyr Leu Met 325 330 335
- Arg Gl μ Leu Pro Phe Gly Ser Asp Gly Val Phe Thr Pro Glu Ala Phe 340 345 350
- Val Glu Arg Thr Asn Phe Asp Leu Ala Asn Asp Leu Gly Asn Leu Val 355 360 365

- Asn Arg Thr Ile Ser Met Val Asn Lys Tyr Phe Asp Gly Glu Leu Pro 370 375 380
- Ala Tyr Gln Gly Pro Leu His Glu Leu Asp Glu Glu Met Glu Ala Met 385 390 395 400
- Ala Leu Glu Thr Val Lys Ser Tyr Thr Glu Ser Met Glu Ser Leu Gln
 405 410 415
- Phe Ser Val Ala Leu Ser Thr Val Trp Lys Phe Ile Ser Arg Thr Asn 420 425 430
- Lys Tyr Ile Asp Glu Thr Thr Pro Trp Val Leu Ala Lys Asp Asp Ser 435 440 445
- Gln Lys Asp Met Leu Gly Asn Val Met Ala His Leu Val Glu Asn Ile 450 455
- Arg Tyr Ala Ala Val Leu Leu Arg Pro Phe Leu Thr His Ala Pro Lys 465 470 475 480
- Glu Ile Phe Glu Gln Leu Asn Ile Asn Asn Pro Gln Phe Met Glu Phe 485 490 495
- Ser Ser Leu Glu Gln Tyr Gly Val Leu Asn Glu Ser Ile Met Val Thr 500 505 510
- Gly Gln Pro Lys Pro Ile Phe Pro Arg Leu Asp Ser Glu Ala Glu Ile 515 520 525
- Ala Tyr Ile Lys Glu Ser Met Gln Pro Pro Ala Thr Lys Glu Glu Lys 530 540
- Glu Glu Ile Pro Ser Lys Pro Gln Ile Asp Ile Lys Asp Phe Asp Lys 545 550 555 560
- Val Glu Ile Lys Ala Ala Thr Ile Ile Asp Ala Glu His Val Lys Lys 565 570 575
- Ser Asp Lys Leu Lys Ile Gln Val Asp Leu Asp Ser Glu Gln Arg
 580 585 590
- Gln Ile Val Ser Gly Ile Ala Lys Phe Tyr Thr Pro Asp Asp Ile Ile 595 600 605
- Gly Lys Lys Val Ala Val Val Thr Asn Leu Lys Pro Ala Lys Leu Met 610 620
- Gly Gln Lys Ser Glu Gly Met Ile Leu Ser Ala Glu Lys Asp Gly Val 625 630 635 640
- Leu Thr Leu Val Ser Leu Pro Ser Ala Ile Pro Asn Gly Ala Val Ile 645 650 655

Lys

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<211> 1974
<212> DNA
<213> Staphylococcus aureus
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ggatatgatg ttcgctattt gactggaacg gatgaacacg gtcaaaaaat tcaagaaaaa 180
gctcaaaaag ctggtaagac agaaattgaa tatttggatg agatgattgc tggaattaaa 240
caattgtggg ctaagcttga aatttcaaat gatgatttta tcagaacaac tgaagaacgt 300
cataaacatg tcgttgagca agtgtttgaa cgtttattaa agcaaggtga tatctattta 360
ggtgaatatg aaggttggta ttctgttccg gatgaaacat actatacaga gtcacaatta 420
gtagacccac aatacgaaaa cggtaaaatt attggtggca aaagtccaga ttctggacac 480
gaagttgaac tagttaaaga agaaagttat ttctttaata ttagtaaata tacagaccgt 540
ttattagagt tctatgacca aaatccagat tttatacaac caccatcaag aaaaaatgaa 600
atgattaaca acttcattaa accaggactt gctgatttag ctgtttctcg tacatcattt 660
aactggggtg tccctgttcc gtctaatcca aaacatgttg tttatgtttg gattgatgcg 720
ttagttaact atatttcagc attaggctat ttatcagatg atgagtcact atttaacaaa 780
tactggccag cagatattca tttaatggct aaggaaattg tgcgattcca ctcaattatt 840
tggcctattt tattgatggc attagactta ccgttaccta aaaaagtctt tgcacatggt 900
tggattttga tgaaagatgg aaaaatgagt aaatctaaag gtaatgtcgt agaccctaat 960
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gcaaatgact taggtaactt agtaaaccgt acgatttcta tggttaataa gtactttgat 1140
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gctttagaaa cagtgaaaag ctacactgaa agcatggaaa gtttgcaatt ttctgtggca 1260
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ttaaaaaattc aagtagactt agattctgaa caaagacaaa ttgtatcagg aattgccaaa 1800
ttctatacac cagatgatat tattggtaaa aaagtagcag ttgttactaa cctgaaaccg 1860
gctaaattaa tgggacaaaa atctgaaggt atgatattat ctgctgaaaa agatggtgta 1920
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<211> 657
<212> PRT
<213> Staphylococcus aureus
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Ile Ala Arg Tyr Lys Arg Met Gln Gly Tyr Asp Val Arg Tyr Leu Thr
Gly Thr Asp Glu His Gly Gln Lys Ile Gln Glu Lys Ala Gln Lys Ala
                         55
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- Gly Lys Thr Glu Ile Glu Tyr Leu Asp Glu Met Ile Ala Gly Ile Lys
 65 70 75 80
- Gln Leu Trp Ala Lys Leu Glu Ile Ser Asn Asp Asp Phe Ile Arg Thr 85 90 95
- Thr Glu Glu Arg His Lys His Val Val Glu Gln Val Phe Glu Arg Leu 100 105 110
- Leu Lys Gln Gly Asp Ile Tyr Leu Gly Glu Tyr Glu Gly Trp Tyr Ser 115 120 125
- Val Pro Asp Glu Thr Tyr Tyr Thr Glu Ser Gln Leu Val Asp Pro Gln 130 135 140
- Tyr Glu Asn Gly Lys Ile Ile Gly Gly Lys Ser Pro Asp Ser Gly His 145 150 155 160
- Glu Val Glu Leu Val Lys Glu Glu Ser Tyr Phe Phe Asn Ile Ser Lys 165 170 175
- Tyr Thr Asp Arg Leu Leu Glu Phe Tyr Asp Gln Asn Pro Asp Phe Ile 180 185 190
- Gln Pro Pro Ser Arg Lys Asn Glu Met Ile Asn Asn Phe Ile Lys Pro 195 200 205
- Gly Leu Ala Asp Leu Ala Val Ser Arg Thr Ser Phe Asn Trp Gly Val 210 215 220
- Pro Val Pro Ser Asn Pro Lys His Val Val Tyr Val Trp Ile Asp Ala 225 230 235 240
- Leu Val Asn Tyr Ile Ser Ala Leu Gly Tyr Leu Ser Asp Asp Glu Ser 245 250 255
- Leu Phe Asn Lys Tyr Trp Pro Ala Asp Ile His Leu Met Ala Lys Glu 260 265 270
- Ile Val Arg Phe His Ser Ile Ile Trp Pro Ile Leu Leu Met Ala Leu 275 280 285
- Asp Leu Pro Leu Pro Lys Lys Val Phe Ala His Gly Trp Ile Leu Met 290 295 300
- Lys Asp Gly Lys Met Ser Lys Ser Lys Gly Asn Val Val Asp Pro Asn 305 310 315 320
- Ile Leu Ile Asp Arg Tyr Gly Leu Asp Ala Thr Arg Tyr Tyr Leu Met
 325 330 335
- Arg Glu Leu Pro Phe Gly Ser Asp Gly Val Phe Thr Pro Glu Ala Phe 340 345 350
- Val Glu Arg Thr Asn Phe Asp Leu Ala Asn Asp Leu Gly Asn Leu Val 355 360 365

Asn	Arg 370	Thr	Ile	Ser	Met	Val 375	Asn	Lys	Tyr	Phe	Asp 380	Gly	Glu	Leu	Pro
Ala 385	Tyr	Gln	Gly	Pro	Leu 390	His	Glu	Leu	Asp	Glu 395	Glu	Met	Glu	Ala	Met 400
Ala	Leu	Glu	Thr	Val 405	Lys	Ser	Tyr	Thr	Glu 410	Ser	Met	Glu	Ser	Leu 415	Gln
Phe	Ser	Val	Ala 420	Leu	Ser	Thr	Val	Trp 425	Lys	Phe	Ile	Ser	Arg 430	Thr	Asn
Lys	Tyr	Ile 435	Asp	Glu	Thr	Thr	Pro 440	Trp	Val	Leu	Ala	Lys 445	Asp	Asp	Ser
Gln	Lys 450	Asp	Met	Leu	Gly	Asn 455	Val	Met	Ala	His	Leu 460	Val	Glu	Asn	Ile
Arg 465	Tyr	Ala	Ala	Val	Leu 470	Leu	Arg	Pro	Phe	Leu 475	Thr	His	Ala	Pro	Lys 480
Glu	Ile	Phe	Glu	Gln 485	Leu	Asn	Ile	Asn	Asn 490	Pro	Gln	Phe	Met	Glu 495	Phe
Ser	Ser	Leu	Glu 500	Gln	Tyr	Gly	Val	Leu 505	Asn	Glu	Ser	Ile	Met 510	Val	Thr
Gly	Gln	Pro 515	Lys	Pro	Ile	Phe	Pro 520	Arg	Leu	Asp	Ser	Glu 525	Ala	Glu	Ile
Ala	Tyr 530	Ile	Lys	Glu	Ser	Met 535	Gln	Pro	Pro	Ala	Thr 540	Lys	Glu	Glu	Lys
Glu 545	Glu	Ile	Pro	Ser	Lys 550	Pro	Gln	Ile	Asp	Ile 555	Lys	Asp	Phe	Asp	Lys. 560
Val	Glu	Ile	Lys	Ala 565	Ala	Thr	Ile	Ile	Asp 570	Ala	Glu	His	Val	Lys 575	Lys
Ser	Asp	Lys	Leu 580	Leu	Lys	Ile	Gln	Val 585	Asp	Leu	Asp	Ser	Glu 590	Gln	Arg
Gln	Ile	Val 595	Ser	Gly	Ile	Ala	Lys 600	Phe	Tyr	Thr	Pro	Asp 605	Asp	Ile	Ile
Gly	Lys 610	Lys	Val	Ala	Val	Val 615	Thr	Asn	Leu	Lys	Pro 620	Ala	Lys	Leu	Met
Gly 625		Lys	Ser	Glu	Gly 630	Met	Ile	Leu	Ser	Ala 635	Glu	Lys	Asp	Gly	Val 640
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<213> Staphylococcus aureus
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Ile Asp Ala Leu Val Asn Tyr Ile Ser Ala Leu Gly Tyr Leu
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<212> PRT
<213> Staphylococcus aureus
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 1
                  5
Ala
<210> 147
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<212> PRT
<213> Staphylococcus aureus
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Asp Ile Tyr Leu Gly Glu
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<213> Staphylococcus aureus
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ccaacggcag atagtttaca tattggtcac ttactaccat tcttaacatt aagacgtttt 180
caagaacatg gacatcgtcc tatcgtttta attggcggtg gtacaggtat gattggtgat 240
ccatcaggta aatcagaaga acgtgtgcta caaacagaag aacaagtaga taaaaatatc 300
gaaggtatta gtaagcaaat gcacaatatt tttgaatttg gaacagacca tggtgcagtg 360
cttgttaata atagagactg gttaggacaa atctcattaa ttagtttttt acgtgactat 420
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acaagtggta ttgaattaat gcgtcgtatg tatggtcaaa cagacgcata cggtttaact 660
attecgettg taactaaate agatggtaag aaatttggta agtetgagte aggtgetgtt 720
tggttagatg ctgaaaaaac aagtccttat gaattttatc aattctggat taatcaatca 780
gacgaagatg taattaaatt cttaaaatac tttactttct taggaaaaga agaaattgat 840
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Gln Gln Thr Asp Glu Gln Gly Ile Glu Asp Leu Leu Asn Lys Glu Gln
Val Thr Leu Tyr Cys Gly Ala Asp Pro Thr Ala Asp Ser Leu His Ile
Gly His Leu Leu Pro Phe Leu Thr Leu Arg Arg Phe Gln Glu His Gly
His Arg Pro Ile Val Leu Ile Gly Gly Gly Thr Gly Met Ile Gly Asp
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- Pro Ser Gly Lys Ser Glu Glu Arg Val Leu Gln Thr Glu Glu Gln Val 85 90 95
- Asp Lys Asn Ile Glu Gly Ile Ser Lys Gln Met His Asn Ile Phe Glu 100 105 110
- Phe Gly Thr Asp His Gly Ala Val Leu Val Asn Asn Arg Asp Trp Leu 115 120 125
- Gly Gln Ile Ser Leu Ile Ser Phe Leu Arg Asp Tyr Gly Lys His Val 130 135 140
- His Gly Ile Ser Tyr Thr Glu Phe Thr Tyr Thr Ile Leu Gln Ala Ile 165 170 175
- Asp Phe Gly His Leu Asn Arg Glu Leu Asn Cys Lys Ile Gln Val Gly
 180 185 190
- Gly Ser Asp Gln Trp Gly Asn Ile Thr Ser Gly Ile Glu Leu Met Arg 195 200 205
- Arg Met Tyr Gly Gln Thr Asp Ala Tyr Gly Leu Thr Ile Pro Leu Val 210 215 220
- Thr Lys Ser Asp Gly Lys Lys Phe Gly Lys Ser Glu Ser Gly Ala Val 225 230 235 240
- Trp Leu Asp Ala Glu Lys Thr Ser Pro Tyr Glu Phe Tyr Gln Phe Trp
 245 250 255
- Ile Asn Gln Ser Asp Glu Asp Val Ile Lys Phe Leu Lys Tyr Phe Thr 260 265 270
- Phe Leu Gly Lys Glu Glu Ile Asp Arg Leu Glu Gln Ser Lys Asn Glu 275 280 285
- Ala Pro His Leu Arg Glu Ala Gln Lys Thr Leu Ala Glu Glu Val Thr 290 295 300
- Lys Phe Ile His Gly Glu Asp Ala Leu Asp Ala Ile Arg Ile Ser 305 310 315 320
- Gln Ala Leu Phe Ser Gly Asp Leu Lys Ser Leu Ser Ala Lys Glu Leu 325 330 335
- Lys Asp Gly Phe Lys Asp Val Pro Gln Val Thr Leu Ser Asn Asp Thr 340 345 350
- Thr Asn Ile Val Glu Val Leu Ile Glu Thr Gly Ile Ser Pro Ser Lys 355 360 365
- Arg Gln Ala Arg Glu Asp Val Asn Asn Gly Ala Ile Tyr Ile Asn Gly 370 375 380

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- His Arg Pro Ile Val Leu Ile Gly Gly Gly Thr Gly Met Ile Gly Asp
 65 70 75 80
- Pro Ser Gly Lys Ser Glu Glu Arg Val Leu Gln Thr Glu Glu Gln Val 85 90 95
- Asp Lys Asn Ile Glu Gly Ile Ser Lys Gln Met His Asn Ile Phe Glu 100 105 110
- Phe Gly Thr Asp His Gly Ala Val Leu Val Asn Asn Arg Asp Trp Leu 115 120 125
- Gly Gln Ile Ser Leu Ile Ser Phe Leu Arg Asp Tyr Gly Lys His Val 130 135 140
- Gly Val Asn Tyr Met Leu Gly Lys Asp Ser Ile Gln Ser Arg Leu Glu 145 150 155 160
- His Gly Ile Ser Tyr Thr Glu Phe Thr Tyr Thr Ile Leu Gln Ala Ile 165 170 175
- Asp Phe Gly His Leu Asn Arg Glu Leu Asn Cys Glu Ile Gln Val Gly
 180 185 190
- Gly Ser Asp Gln Trp Gly Asn Ile Thr Ser Gly Ile Glu Leu Met Arg 195 200 205
- Arg Met Tyr Gly Gln Thr Asp Ala Tyr Gly Leu Thr Ile Pro Leu Val 210 215 220
- Thr Lys Ser Asp Gly Lys Lys Phe Gly Lys Ser Glu Ser Gly Ala Val 225 230 235 240
- Trp Leu Asp Ala Glu Lys Thr Ser Pro Tyr Glu Phe Tyr Gln Phe Trp
 245 250 255
- Ile Asn Gln Ser Asp Glu Asp Val Ile Lys Phe Leu Lys Tyr Phe Thr 260 265 270
- Phe Leu Gly Lys Glu Glu Ile Asp Arg Leu Glu Gln Ser Lys Asn Glu 275 280 285
- Ala Pro His Leu Arg Glu Ala Gln Lys Thr Leu Ala Glu Glu Val Thr 290 295 300
- Lys Phe Ile His Gly Glu Asp Ala Leu Asn Asp Ala Ile Arg Ile Ser 305 310 315 320
- Gln Ala Leu Phe Ser Gly Asp Leu Lys Ser Leu Ser Ala Lys Glu Leu 325 330 335
- Lys Asp Gly Phe Lys Asp Val Pro Gln Val Thr Leu Ser Asn Asp Thr 340 345 350
- Thr Asn Ile Val Glu Val Leu Ile Glu Thr Gly Ile Ser Pro Ser Lys 355 360 365

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Arg Gln Ala Arg Glu Asp Val Asn Asn Gly Ala Ile Tyr Ile Asn Gly
    370
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ccaatttttg aaagtacaga tetttttgca agaggtgttg gtgattcaac egatgtegta 180
caaaaagaaa tgtatacatt taaagataaa ggcgatagaa gtattacatt aagacctgag 240
ggaacagctg cagttgtgcg ttcatatatt gaacataaaa tgcaaggtaa tccaaaccaa 300
ccaattaaac tttattacaa tggaccgatg tttagatatg aacgtaagca aaaaggacgc 360
tatcgtcaat ttaatcaatt tggtgtagaa gctattggtg ctgaaaatcc tagcgtagat 420
qcaqaaqtat tagctatggt tatgcatatt tatcaatcat ttggattaaa acatttaaag 480
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Phe Ala Arg Gly Val Gly Asp Ser Thr Asp Val Val Gln Lys Glu Met
                        55
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Tyr Thr Phe Lys Asp Lys Gly Asp Arg Ser Ile Thr Leu Arg Pro Glu Gly Thr Ala Ala Val Val Arg Ser Tyr Ile Glu His Lys Met Gln Gly Asn Pro Asn Gln Pro Ile Lys Leu Tyr Tyr Asn Gly Pro Met Phe Arg Tyr Glu Arg Lys Gln Lys Gly Arg Tyr Arg Gln Phe Asn Gln Phe Gly Val Glu Ala Ile Gly Ala Glu Asn Pro Ser Val Asp Ala Glu Val Leu 135 Ala Met Val Met His Ile Tyr Gln Ser Phe Gly Leu Lys His Leu Lys 150 Leu Val Ile Asn Ser Val Gly Asp Met Ala Ser Arg Lys Glu Tyr Asn Glu Ala Leu Val Lys His Phe Glu Pro Val Ile His Glu Phe Cys Ser 185 Asp Cys Gln Ser Arg Leu His Thr Asn Pro Met Arg Ile Leu Asp Cys 195 200 Lys Val Asp Arg Asp Lys Glu Ala Ile Lys Thr Ala Pro Arg Ile Thr 215 Asp Phe Leu Asn Glu Glu Ser Lys Ala Tyr Tyr Glu Gln Val Lys Ala Tyr Leu Asp Asp Leu Gly Ile Pro Tyr Ile Glu Asp Pro Asn Leu Val Arg Gly Leu Asp Tyr Tyr Thr His Thr Ala Phe Glu Leu Met Met Asp 265 Asn Pro Asn Tyr Asp Gly Ala Ile Thr Thr Leu Cys Gly Gly Gly Arg Tyr Asn Gly Leu Leu Glu Leu Leu Asp Gly Pro Ser Glu Thr Gly Ile Gly Phe Ala Leu Ser Ile Glu Arg Leu Leu Leu Ala Leu Glu Glu Glu 305 Gly Ile Glu Leu Asp Ile Glu Glu Asn Leu Asp Leu Phe Ile Val Thr 330 Met Gly Asp Gln Ala Asp Arg Tyr Ala Val Lys Leu Leu Asn His Leu

Arg His Asn Gly Ile Lys Ala Asp Lys Asp Tyr Leu Gln Arg Lys Ile 355 360 365

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Lys Gly Gln Met Lys Gln Ala Asp Arg Leu Gly Ala Lys Phe Thr Ile
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Met Thr Thr Gly Glu Ser Glu Thr Ile Glu Leu Asp Ala Leu Val Glu
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Tyr Phe Lys Lys
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caaaaagaaa tgtatacatt taaagataaa ggcgatagaa gtattacatt aagatctgaa 240
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aaagactatt tacagcgtaa aattaaagga caaatgaaac aagcagaccg tttaggtgcc 1140
aagtttacaa tcgttattgg tgatcaagaa ttagaaaata ataaaatcga tgttaaaaat 1200
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<213> Staphylococcus aureus
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Lys Lys Trp Arg Tyr Ile Glu Asn Gln Leu Asp Glu Leu Met Thr Phe
Tyr Asn Tyr Lys Glu Ile Arg Thr Pro Ile Phe Glu Ser Thr Asp Leu
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- Phe Ala Arg Gly Val Gly Asp Ser Thr Asp Val Val Gln Lys Glu Met 50 55 60
- Tyr Thr Phe Lys Asp Lys Gly Asp Arg Ser Ile Thr Leu Arg Ser Glu 65 70 75 80
- Gly Thr Ala Ala Val Val Arg Ser Tyr Ile Glu His Lys Met Gln Gly 85 90 95
- Asn Pro Asn Gln Pro Ile Lys Leu Tyr Tyr Asn Gly Pro Met Phe Arg
- Tyr Glu Arg Lys Gln Lys Gly Arg Tyr Arg Gln Phe Asn Gln Phe Gly 115 120 125
- Val Glu Ala Ile Gly Ala Glu Asn Pro Ser Val Asp Ala Glu Val Leu 130 140
- Ala Met Val Met His Ile Tyr Gln Ser Phe Gly Leu Lys His Leu Lys 145 150 155 160
- Ile Val Ile Asn Ser Val Gly Asp Met Ala Ser Arg Lys Glu Tyr Asn 165 170 175
- Glu Ala Leu Val Lys His Phe Glu Pro Val Ile His Glu Phe Cys Ser 180 185 190
- Asp Cys Gln Ser Arg Leu His Thr Asn Pro Met Arg Ile Leu Asp Cys 195 200 205
- Lys Val Asp Arg Asp Lys Glu Ala Ile Lys Thr Ala Pro Arg Ile Thr 210 215 220
- Asp Phe Leu Asn Glu Glu Ser Lys Ala Tyr Tyr Glu Gln Val Lys Ala 225 230 235 240
- Tyr Leu Asp Asp Leu Gly Ile Pro Tyr Ile Glu Asp Pro Asn Leu Val 245 250 255
- Arg Gly Leu Asp Tyr Tyr Thr His Thr Ala Phe Glu Leu Met Met Asp 260 270
- Asn Pro Asn Tyr Asp Gly Ala Ile Thr Thr Leu Cys Gly Gly Gly Arg 275 280 285
- Tyr Asn Gly Leu Leu Glu Leu Leu Asp Gly Pro Ser Glu Thr Gly Ile 290 295 300
- Gly Phe Ala Leu Ser Ile Glu Arg Leu Leu Leu Ala Leu Glu Glu 305 310 315 320
- Gly Ile Glu Leu Asp Ile Glu Glu Asn Leu Asp Leu Phe Ile Val Thr 325 330 335
- Met Gly Asp Gln Ala Asp Arg Tyr Ala Val Lys Leu Leu Asn His Leu 340 345 350

355 360 365													
Lys Gly Gln Met Lys Gln Ala Asp Arg Leu Gly Ala Lys Phe Thr Ile 370 375 380													
Val Ile Gly Asp Gln Glu Leu Glu Asn Asn Lys Ile Asp Val Lys Asn 385 390 395 400													
Ile Thr Thr Gly Glu Ser Glu Thr Ile Glu Leu Asp Ala Leu Val Glu 405 410 415													
Tyr Phe Lys Lys 420													
<210> 161 <211> 33 <212> DNA <213> Artificial Sequence													
<220> <223> Description of Artificial Sequence: Synthetic primer													
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Gln Ser Phe Gly Leu Lys His Leu Lys Leu Val Ile Asn Ser 20 25 30													

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<213> Staphylococcus aureus
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<213> Staphylococcus aureus
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ttaaaggtca taccagcttt aaaagaaggt aaggttgtgt tgtgtgatcg ctatatcgat 300
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aacgaatttg caataaatgg attatatcca gacttgacga tttatttaaa tgttagtgct 420
gaagtaggtc gcgaacgtat tattaaaaat tcaagagatc aaaatagatt agatcaagaa 480
gatttaaagt ttcacgaaaa agtaattgaa ggttaccaag aaatcattca taatgaatca 540
caacggttca aaagcgttaa tgcagatcaa cctcttgaaa atgttgttga agacacgtat 600
caaactatca tcaaatattt agaaaagata tga
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<212> PRT
<213> Staphylococcus aureus
<400> 167
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Gly Ser Gly Lys Thr Thr Val Ile Asn Glu Val Tyr His Arg Leu Val
Lys Asp Tyr Asp Val Ile Met Thr Arg Glu Pro Gly Gly Val Pro Thr
        35
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Arg Thr Glu Ala Met Leu Phe Ala Ala Ser Arg Arg Glu His Leu Val
Leu Lys Val Ile Pro Ala Leu Lys Glu Gly Lys Val Val Leu Cys Asp
                                     90
Arg Tyr Ile Asp Ser Ser Leu Ala Tyr Gln Gly Tyr Ala Arg Gly Ile
Gly Val Glu Val Arg Ala Leu Asn Glu Phe Ala Ile Asn Gly Leu
                            120
Tyr Pro Asp Leu Thr Ile Tyr Leu Asn Val Ser Ala Glu Val Gly Arg
                        135
Glu Arg Ile Ile Lys Asn Ser Arg Asp Gln Asn Arg Leu Asp Gln Glu
Asp Leu Lys Phe His Glu Lys Val Ile Glu Gly Tyr Gln Glu Ile Ile
His Asn Glu Ser Gln Arg Phe Lys Ser Val Asn Ala Asp Gln Pro Leu
Glu Asn Val Val Glu Asp Thr Tyr Gln Thr Ile Ile Lys Tyr Leu Glu
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                                                205
Lys Ile
    210
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<213> Staphylococcus aureus
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agagaaccag gtggtgttcc tactggtgaa gaaatacgta aaattgtatt agaaggcaat 180
gatatggaca ttagaactga agcaatgtta tttgctgcat ctagaagaga acatcttgta 240
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agttcattag cttatcaagg ttatgctaga gggattggcg ttgaagaagt aagagcatta 360
aacgaatttg caataaatgg attatatcca gacttgacga tttatttaaa tgttagtgct 420
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gatttaaagt ttcacgaaaa agtaattgaa ggttaccaag aaatcattca taatgaatca 540
caacggttca aaagcgttaa tgcagatcaa cctcttgaaa atgttgttga agacacgtat 600
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633

caaactatca tcaaatattt agaaaagata tga

<210> 169

<211> 210

<212> PRT

<213> Staphylococcus aureus

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Lys Asp Tyr Asp Val Ile Met Thr Arg Glu Pro Gly Gly Val Pro Thr 35 40 45

Gly Glu Glu Ile Arg Lys Ile Val Leu Glu Gly Asn Asp Met Asp Ile 50 55 60

Arg Thr Glu Ala Met Leu Phe Ala Ala Ser Arg Glu His Leu Val
65 70 75 80

Leu Lys Val Ile Pro Ala Leu Lys Glu Gly Lys Val Val Leu Cys Asp 85 90 95

Arg Tyr Ile Asp Ser Ser Leu Ala Tyr Gln Gly Tyr Ala Arg Gly Ile 100 105 110

Gly Val Glu Glu Val Arg Ala Leu Asn Glu Phe Ala Ile Asn Gly Leu 115 120 125

Tyr Pro Asp Leu Thr Ile Tyr Leu Asn Val Ser Ala Glu Val Gly Arg 130 135 140

Glu Arg Ile Ile Lys Asn Ser Arg Asp Gln Asn Arg Leu Asp Gln Glu 145 150 155 160

Asp Leu Lys Phe His Glu Lys Val Ile Glu Gly Tyr Gln Glu Ile Ile 165 170 175

His Asn Glu Ser Gln Arg Phe Lys Ser Val Asn Ala Asp Gln Pro Leu 180 185 190

Glu Asn Val Val Glu Asp Thr Tyr Gln Thr Ile Ile Lys Tyr Leu Glu 195 200 205

Lys Ile 210

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<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
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<213> Staphylococcus aureus
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<212> DNA
<213> Staphylococcus aureus
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ttacaaaaaa ctgtagatgt ttatcgtaac tataaagcta aaaaagaaga attagctgat 180
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cctaaagatc ctaatgatga caaagacgtt attgtagaaa taagagcagc agcaggtggt 360
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caaggattca aaactgaaat agtagaagcg tctgaaagtg accatggtgg ttacaaagaa 480
attagtttct cagtttctgg taatggcgcg tatagtaaat tgaaatttga aaatggtgcg 540
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Lys Tyr Ser Lys Glu Gln Ala Asp Leu Gln Lys Thr Val Asp Val Tyr
Arg Asn Tyr Lys Ala Lys Lys Glu Glu Leu Ala Asp Ile Glu Glu Met
Leu Ser Glu Thr Asp Asp Lys Glu Glu Val Glu Met Leu Lys Glu Glu
Ser Asn Gly Ile Lys Ala Glu Leu Pro Asn Leu Glu Glu Glu Leu Lys
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Ile Leu Leu Ile Pro Lys Asp Pro Asn Asp Asp Lys Asp Val Ile Val
Glu Ile Arg Ala Ala Ala Gly Gly Asp Glu Ala Ala Ile Phe Ala Gly
Asp Leu Met Arg Met Tyr Ser Lys Tyr Ala Glu Ser Gln Gly Phe Lys
Thr Glu Ile Val Glu Ala Ser Glu Ser Asp His Gly Gly Tyr Lys Glu
Ile Ser Phe Ser Val Ser Gly Asn Gly Ala Tyr Ser Lys Leu Lys Phe
Glu Asn Gly Ala His Arg Val Gln Arg Val Pro Glu Thr Glu Ser Gly
Gly Arg Ile His Thr Ser Thr Ala Thr Val Ala Val Leu Pro Glu Val
                            200
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Glu Asp Val Glu Ile Glu Ile Arg Asn Glu Asp Leu Lys Ile Asp Thr

220

215

210

Tyr Arg Ser Ser Gly Ala Gly Gln His Val Asn Thr Thr Asp Ser Ala Val Arg Ile Thr His Leu Pro Thr Gly Val Ile Ala Thr Ser Ser 245 250 Glu Lys Ser Gln Ile Gln Asn Arg Glu Lys Ala Met Lys Val Leu Lys Ala Arg Leu Tyr Asp Met Lys Val Gln Glu Gln Gln Lys Tyr Ala 280 Ser Gln Arg Lys Ser Ala Val Gly Thr Gly Asp Arg Ser Glu Arg Ile Arg Thr Tyr Asn Tyr Pro Gln Ser Arg Val Thr Asp His Arg Ile Gly 310 315 Leu Thr Leu Gln Lys Leu Gly Gln Ile Met Glu Gly His Leu Glu Glu Ile Ile Asp Ala Leu Thr Leu Ser Glu Gln Thr Asp Lys Leu Lys Glu 345 Leu Asn Asn Gly Glu Leu 355 <210> 177 <211> 1077

<212> DNA <213> Staphylococcus aureus

<400> 177

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- <211> 358
- <212> PRT
- <213> Staphylococcus aureus
- <400> 178
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- Glu Leu Leu Ser Asp Pro Asp Val Val Asn Asp Ser Asp Lys Leu Arg
- Lys Tyr Ser Lys Glu Gln Ala Asp Leu Gln Lys Thr Val Asp Val Tyr 35 40 45
- Arg Asn Tyr Lys Ala Lys Lys Glu Glu Leu Ala Asp Ile Glu Glu Met 50 60
- Leu Ser Glu Thr Asp Asp Lys Glu Glu Val Glu Met Leu Lys Glu Glu 65 70 75 80
- Ser Asn Gly Ile Lys Ala Glu Leu Pro Asn Leu Glu Glu Glu Leu Lys 85 90 95
- Ile Leu Leu Ile Pro Lys Asp Pro Asn Asp Asp Lys Asp Val Ile Val
- Glu Ile Arg Ala Ala Ala Gly Gly Asp Glu Ala Ala Ile Phe Ala Gly 115 120 125
- Asp Leu Met Arg Met Tyr Ser Lys Tyr Ala Glu Ser Gln Gly Phe Lys 130 140
- Thr Glu Ile Val Glu Ala Ser Glu Ser Asp His Gly Gly Tyr Lys Glu 145 , 150 155 160
- Ile Ser Phe Ser Val Ser Gly Asn Gly Ala Tyr Ser Lys Leu Lys Phe
 165 170 175
- Glu Asn Gly Ala His Arg Val Gln Arg Val Pro Glu Thr Glu Ser Gly 180 185 190
- Gly Arg Ile His Thr Ser Thr Ala Thr Val Ala Val Leu Pro Glu Val 195 200 205
- Glu Asp Val Glu Ile Glu Ile Arg Asn Glu Asp Leu Lys Ile Asp Thr 210 215 220
- Tyr Arg Ser Ser Gly Ala Gly Gly Gln His Val Asn Thr Thr Asp Ser 225 230 235 240
- Ala Val Arg Ile Thr His Leu Pro Thr Gly Val Ile Ala Thr Ser Ser 245 250 255
- Glu Lys Ser Gln Ile Gln Asn Arg Glu Lys Ala Met Lys Val Leu Lys 260 265 270

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Ser Gln Arg Lys Ser Ala Val Gly Thr Gly Asp Arg Ser Glu Arg Ile
Arg Thr Tyr Asn Tyr Pro Gln Ser Arg Val Thr Asp His Cys Ile Gly
305
                    310
                                        315
Leu Thr Leu Gln Lys Leu Gly Gln Ile Met Glu Gly His Leu Glu Glu
Ile Ile Asp Ala Leu Thr Leu Ser Glu Gln Thr Asp Lys Leu Lys Glu
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Leu Asn Asn Gly Glu Leu
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<213> Staphylococcus aureus
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<213> Staphylococcus aureus
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Met Lys Val Leu Lys Ala Arg
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<212> DNA
<213> Streptococcus pneumoniae
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acgcctattt ttgagcatta cgaggttatc agtcgctctg tcggagatac aacggatatc 180
gtaaccaagg aaatgtacga tttttatgac aagggtgacc gtcatattac cctccgtcca 240
gaaggaactg caccegttgt cegttectat gtggaaaata aacttttege cecagaagtg 300
caaaagccaa gcaagttcta ctacatggga cctatgttcc gttatgagcg tccacaqqca 360
gggcgcttgc gccaattcca ccagattggt gttgagtgtt ttggctctag caatccagct 420
accgatgtgg aaacaatcgc tatggcagcc cattttttga aggaaatcgg tattcaaggt 480
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ttgattgact atttgacacc getcaaggag acettgteta aggatageca aegtegettg 600
gaggaaaatc ctcttcgtgt cttggactct aaggaaaaag aagacaaggt ggcagtagag 660
aatgegeegt etatettgga etttettgat gaagaaagee aageteattt tgatgetgtg 720
cgtcagatgt tggaaaatct tggagtagat tacatcatcg ataccaatat ggtgcgtggt 780
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gctggatttg gttttggact tggtgtagag cgcctgcttc tcatccttqa aaaqcaaqqt 960
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                                                                   1290
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<211> 429
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<213> Streptococcus pneumoniae
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- Arg Tyr Asn Tyr Ala Glu Val Arg Thr Pro Ile Phe Glu His Tyr Glu 35 40 45
- Val Ile Ser Arg Ser Val Gly Asp Thr Thr Asp Ile Val Thr Lys Glu 50 55 60
- Met Tyr Asp Phe Tyr Asp Lys Gly Asp Arg His Ile Thr Leu Arg Pro 65 70 75 80
- Glu Gly Thr Ala Pro Val Val Arg Ser Tyr Val Glu Asn Lys Leu Phe \$85\$ 90 95
- Ala Pro Glu Val Gln Lys Pro Ser Lys Phe Tyr Tyr Met Gly Pro Met 100 105 110
- Phe Arg Tyr Glu Arg Pro Gln Ala Gly Arg Leu Arg Gln Phe His Gln 115 120 125
- Ile Gly Val Glu Cys Phe Gly Ser Ser Asn Pro Ala Thr Asp Val Glu 130 135 140
- Thr Ile Ala Met Ala Ala His Phe Leu Lys Glu Ile Gly Ile Gln Gly 145 150 155 160
- Val Lys Leu His Leu Asn Thr Leu Gly Asn Pro Glu Ser Arg Ala Ala 165 170 175
- Tyr Arg Gln Ala Leu Ile Asp Tyr Leu Thr Pro Leu Lys Glu Thr Leu 180 185 190
- Ser Lys Asp Ser Gln Arg Arg Leu Glu Glu Asn Pro Leu Arg Val Leu 195 200 205
- Asp Ser Lys Glu Lys Glu Asp Lys Val Ala Val Glu Asn Ala Pro Ser 210 220
- Ile Leu Asp Phe Leu Asp Glu Glu Ser Gln Ala His Phe Asp Ala Val 225 230 235 240
- Arg Gln Met Leu Glu Asn Leu Gly Val Asp Tyr Ile Ile Asp Thr Asn 245 250 255
- Met Val Arg Gly Leu Asp Tyr Tyr Asn His Thr Ile Phe Glu Phe Ile 260 265 270
- Thr Glu Ile Glu Gly Asn Asp Leu Thr Val Cys Ala Gly Gly Arg Tyr 275 280 285
- Asp Gly Leu Val Ala Tyr Phe Gly Gly Pro Glu Thr Ala Gly Phe Gly 290 295 300
- Phe Gly Leu Gly Val Glu Arg Leu Leu Leu Ile Leu Glu Lys Gln Gly 305 310 315 320

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Gln Gln Gly Phe Lys Ala Glu Arg Asp Tyr Leu Asn Arg Lys Leu Lys
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Leu Gly Glu Ser Glu Val Glu Ser Gly Gln Val Thr Val Lys Asn Asn
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gaggaaaatc ctcttcgtgt cttggactct aaggaaaaag aagacaaggt ggctgtagag 660
aatgegeeat etatettgga ttteettgat gaagaaagte aageteattt tgatgetgtg 720
cgtcagatgt tggaaaatct tggagtagac tacatcatcg ataccaatat ggtgcgtggt 780
ctggactact acaaccacac cattttcgag tttatcacag agattgaggg caatgacttg 840
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1290

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<211> 429

<212> PRT

<213> Streptococcus pneumoniae

-400× 187

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Arg Tyr Asn Tyr Ala Glu Val Arg Thr Pro Ile Phe Glu His Tyr Glu 35 40 45

Val Ile Ser Arg Ser Val Gly Asp Thr Thr Asp Ile Val Thr Lys Glu 50 55 60

Met Tyr Asp Phe Tyr Asp Lys Gly Asp Arg His Ile Thr Leu Arg Pro 65 70 75 80

Glu Gly Thr Ala Pro Val Val Arg Ser Tyr Val Glu Asn Lys Leu Phe
85 90 95

Ala Pro Glu Val Gln Lys Pro Ser Lys Phe Tyr Tyr Met Gly Pro Met
100 105 110

Phe Arg Tyr Glu Arg Pro Gln Ala Gly Arg Leu Arg Gln Phe His Gln
115 120 125

Ile Gly Val Glu Cys Phe Gly Ser Ser Asn Pro Ala Thr Asp Val Glu 130 135 140

Thr Ile Val Met Ala Ala His Phe Leu Lys Glu Ile Gly Ile Gln Gly 145 150 155 160

Val Lys Leu His Leu Asn Thr Leu Gly Asn Pro Glu Ser Arg Ala Ala 165 170 175

Tyr Arg Gln Ala Leu Ile Asp Tyr Leu Thr Pro Leu Lys Glu Thr Leu 180 185 190

Ser Lys Asp Ser Gln Arg Arg Leu Glu Glu Asn Pro Leu Arg Val Leu 195 200 205

Asp Ser Lys Glu Lys Glu Asp Lys Val Ala Val Glu Asn Ala Pro Ser 210 215 220

Ile Leu Asp Phe Leu Asp Glu Glu Ser Gln Ala His Phe Asp Ala Val 225 230 235 240

Arg Gln Met Leu Glu Asn Leu Gly Val Asp Tyr Ile Ile Asp Thr Asn 245 250 255

Met Val Arg Gly Leu Asp Tyr Tyr Asn His Thr Ile Phe Glu Phe Ile 260 265 270

Thr Glu Ile Glu Gly Asn Asp Leu Thr Ile Cys Ala Gly Gly Arg Tyr
275 280 285

Asp Gly Leu Val Ala Tyr Phe Gly Gly Pro Glu Thr Ala Gly Phe Gly 290 295 300

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Val A	Ala	Leu	Pro	Ile 325	Glu	Asn	Ala	Leu	Asp 330	Val	Tyr	Ile	Ala	Val 335	Leu	
Gly A	Asp	Gly	Ala 340	Asn	Val	Lys	Ala	Leu 345	Glu	Leu	Val	Gln	Val 350	Leu	Arg	
Gln (Gln	Gly 355	Phe	Lys	Ala	Glu	Arg 360	Asp	Tyr	Leu	Asn	Arg 365	Lys	Leu	Lys	`
Ala (Gln 370	Phe	Lys	Ser	Ala	Asp 375	Val	Phe	Ala	Ala	Lys 380	Thr	Leu	Ile	Thr	
Leu (Gly	Glu	Ser	Glu	Val 390	Glu	Ser	Gly	Gln	Val 395	Thr	Val	Lys	Asn	Asn 400	
Gln T	Thr	Arg	Glu	Glu 405	Val	Gln	Val	Ser	Leu 410	Glu	Thr	Ile	Ser	Gln 415	Asn	
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<400> 191
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<211> 13
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                  5
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- <210> 194
- <211> 311
- <212> PRT
- <213> Streptococcus pneumoniae

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- Tyr Ile Ser Gly Glu Lys Ile Ala Glu Lys Leu Ser Leu Ser Arg Thr
 20 25 30
- Ala Ile Trp Lys Ala Ile Lys Arg Leu Glu Gln Glu Gly Ile Glu Ile
 35 40 45
- Asp Ser Ile Lys Asn Arg Gly Tyr Lys Leu Met Asn Gly Asp Leu Ile 50 55 60
- Leu Pro Glu Ile Leu Glu Glu Asn Leu Pro Ile Lys Val Ser Phe Lys 65 70 75 80
- Pro Glu Thr Lys Ser Thr Gln Leu Asp Ala Lys Glu Ala Ile Asp Leu 85 90 95
- Gly His Glu Ala Asn Thr Leu Tyr Leu Ala Ser Tyr Gln Thr Ala Gly
 100 105 110
- Arg Gly Arg Phe Gln Arg Ser Phe Tyr Ser Pro Gln Gly Gly Ile Tyr
 115 120 125
- Met Thr Leu His Leu Lys Pro Asn Leu Pro Tyr Asp Lys Leu Pro Ser 130 135 140
- Thr Leu Ile Asp Val Asp Ile Lys Trp Val Asn Asp Ile Tyr Leu Asn 165 170 175
- Asn His Lys Ile Gly Gly Ile Leu Thr Glu Ala Met Thr Ser Val Glu
 180 185 190
- Thr Gly Leu Val Thr Asp Ile Ile Gly Val Gly Ile Asn Phe Thr 195 200 205
- Ile Lys Asp Phe Pro Gln Glu Leu Lys Glu Lys Ala Ala Ser Leu Phe 210 215 220
- Lys Ala Thr Ala Pro Ile Thr Arg Asn Glu Leu Ile Ile Glu Ile Trp 225 230 235 240
- Arg Ala Phe Phe Glu Thr Pro Ala Glu Glu Leu Leu Tyr Leu Tyr Lys
 245 250 255
- Lys Gln Ser Phe Ile Leu Gly Lys Glu Val Thr Phe Thr Leu Glu Gln 260 265 270

Lys Asp Tyr Lys Gly Leu Ala Lys Asp Ile Ser Glu Asn Gly Lys Leu 280 Leu Val Gln Cys Asp Asn Gly Lys Glu Ile Trp Leu Asn Ser Gly Glu 295 Ile Ser Leu Asn Ser Trp Lys 305 310 <210> 195 <211> 936 <212> DNA <213> Streptococcus pneumoniae <400> 195 atgaaatcct accaagctgt ctaccaaatc ctatctaaag aaaccgacta tatcagcgga 60 gaaaaaatcg cagaaaaact atccctaagc cgaacagcaa tttggaaagc catcaagcga 120 ctagaacaag aaggcattga aattgatagt atcaaaaata gaggatataa actgatgaat 180 ggtgacctta ttcttccaga gattctagaa gaaaatcttc caattaaagt cagctttaaa 240 cccqaaacaa aatcaacaca actagatgca aaagaagcaa ttgatttagg ccatgaagca 300 aataccctct atctagcttc ctatcaaaca gcaggccgag gccgttttca acgttccttc 360 tactcaccac aaggtggtat ttatatgaca ctccatctta aaccaaatct cccctatgac 420 aaattaccat cctacacact acttgtagct ggagctgtct acaaagccat taagaaccta 480 actttaatag atgtcgacat aaaatgggtc aatgatatct atctaaacaa tcataaaatt 540 ggaggaatcc ttactgaagc aatgacctct gtagaaactg gcttagtcac agatatcatt 600 attggagtag gtatcaattt cactattaaa gacttccctc aggaattaaa agaaaaagct 660 gccagcttat ttaaagctac agctcctata acaaggaatg aattgatcat agaaatctgg 720 cgtactttct tcgaaacacc agcagaagag ctattatacc tatacaaaaa acagtcattc 780 attctaggaa aagaagtcac tttcacacta gagcaaaaag actacaaggg acttgctaaa 840 qacatctcaq aaaatqqaaa acttttagtt caatgtgata acggaaaaga aatctggcta 900 aatagtggcg aaatttctct caatagttgg aagtaa <210> 196 <211> 311 <212> PRT <213> Streptococcus pneumoniae <400> 196 Met Lys Ser Tyr Gln Ala Val Tyr Gln Ile Leu Ser Lys Glu Thr Asp Tyr Ile Ser Gly Glu Lys Ile Ala Glu Lys Leu Ser Leu Ser Arg Thr Ala Ile Trp Lys Ala Ile Lys Arg Leu Glu Gln Glu Gly Ile Glu Ile Asp Ser Ile Lys Asn Arg Gly Tyr Lys Leu Met Asn Gly Asp Leu Ile Leu Pro Glu Ile Leu Glu Glu Asn Leu Pro Ile Lys Val Ser Phe Lys Pro Glu Thr Lys Ser Thr Gln Leu Asp Ala Lys Glu Ala Ile Asp Leu 90

Gly His Glu Ala Asn Thr Leu Tyr Leu Ala Ser Tyr Gln Thr Ala Gly
100 105 110

Arg Gly Arg Phe Gln Arg Ser Phe Tyr Ser Pro Gln Gly Gly Ile Tyr 115 120 125

Met Thr Leu His Leu Lys Pro Asn Leu Pro Tyr Asp Lys Leu Pro Ser 130 135 140

Tyr Thr Leu Leu Val Ala Gly Ala Val Tyr Lys Ala Ile Lys Asn Leu 145 150 155 160

Thr Leu Ile Asp Val Asp Ile Lys Trp Val Asn Asp Ile Tyr Leu Asn 165 170 175

Asn His Lys Ile Gly Gly Ile Leu Thr Glu Ala Met Thr Ser Val Glu 180 $$185\$

Thr Gly Leu Val Thr Asp Ile Ile Gly Val Gly Ile Asn Phe Thr 195 200 205

Ile Lys Asp Phe Pro Gln Glu Leu Lys Glu Lys Ala Ala Ser Leu Phe 210 215 220

Lys Ala Thr Ala Pro Ile Thr Arg Asn Glu Leu Ile Ile Glu Ile Trp 225 230 235 240

Arg Thr Phe Phe Glu Thr Pro Ala Glu Glu Leu Leu Tyr Leu Tyr Lys 245 250 255

Lys Gln Ser Phe Ile Leu Gly Lys Glu Val Thr Phe Thr Leu Glu Gln 260 265 270

Lys Asp Tyr Lys Gly Leu Ala Lys Asp Ile Ser Glu Asn Gly Lys Leu 275 280 285

Leu Val Gln Cys Asp Asn Gly Lys Glu Ile Trp Leu Asn Ser Gly Glu 290 295 300

Ile Ser Leu Asn Ser Trp Lys 305 310

<210> 197

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 197

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<400> 198
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<210> 199
<211> 41
<212> PRT
<213> Streptococcus pneumoniae
<400> 199
Tyr Met Thr Leu His Leu Lys Pro Asn Leu Pro Tyr Asp Lys Leu Pro
Ser Tyr Thr Leu Leu Val Ala Gly Ala Val Tyr Lys Ala Ile Lys Asn
Leu Thr Leu Ile Asp Val Asp Ile Lys
<210> 200
<211> 7
<212> PRT
<213> Streptococcus pneumoniae
<400> 200
Lys Leu Leu Val Gln Cys Asp
<210> 201
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<212> PRT
<213> Streptococcus pneumoniae
<400> 201
Tyr Gln Ala Val Tyr Gln Ile Leu Ser
<210> 202
<211> 1077
<212> DNA
<213> Streptococcus pneumoniae
<400> 202
atgggatata cagttgctgt agtcggcgcg acaggtgctg tcggtgctca gatgataaaa 60
atgttggaag aatcaacact tccaatcgat aaaattcgtt accttgcttc tgcacgttca 120
gcaggtaagt cattgaaatt taaagatcaa gatattacaa ttgaagaaac gactgaaaca 180
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gcttttgaag gagttgatat tgctctcttt tcagcaggta gttctacatc agctaagtat 240

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gcaccatacg cagtaaaagc tggcgtggta gtagtagata atacatctta tttccgtcaa 300
aatccagatg ttcctttggt tgttccagag gtcaatgctc atgcacttga tgctcacaac 360
ggaatcattg cctgccctaa ttgttcaaca attcaaatga tggtggctct tgagccggtt 420
cgccaaaaat ggggcttgga ccgtatcatt gtttcaactt atcaagccgt ttcaggtgct 480
ggtatgggag caattettga gacacaacgt gaacttegtg aagtettgaa tgatggtgtg 540
aaaccacgtg atttgcatgc ggaaatcttg ccttcaggtg gtgacaagaa acattatcct 600
ategeettta aegetettee acaaattgat gtttteaetg ataatgatta caegtaegaa 660
gagatgaaga tgaccaagga aactaagaaa attatggaag atgatagcat tgcagtatct 720
gcaacatgtg tgcgtattcc agtcttgtca gctcactctg agtctgttta tatcgaaaca 780
aaagaagtgg ctccaatcga agaagtaaaa gcagctatcg cagccttccc aggtgctgtt 840
cttgaagatg atgtagctca tcaaatctat cctcaagcta tcaatgcagt tggttcgcgt 900
gatacetttg ttggtcgtat ccgtaaagac ttggatgcag aaaaaggaat tcacatgtgg 960
gttgtttcag ataaccttct caaaggtgct gcttggaact cagttcagat tgctgaaact 1020
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<210> 203
<211> 358
<212> PRT
<213> Streptococcus pneumoniae
<400> 203
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Gln Met Ile Lys Met Leu Glu Glu Ser Thr Leu Pro Ile Asp Lys Ile
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Arg Tyr Leu Ala Ser Ala Arg Ser Ala Gly Lys Ser Leu Lys Phe Lys
Asp Gln Asp Ile Thr Ile Glu Glu Thr Thr Glu Thr Ala Phe Glu Gly
Val Asp Ile Ala Leu Phe Ser Ala Gly Ser Ser Thr Ser Ala Lys Tyr
Ala Pro Tyr Ala Val Lys Ala Gly Val Val Val Asp Asn Thr Ser
                                     90
Tyr Phe Arg Gln Asn Pro Asp Val Pro Leu Val Val Pro Glu Val Asn
Ala His Ala Leu Asp Ala His Asn Gly Ile Ile Ala Cys Pro Asn Cys
Ser Thr Ile Gln Met Met Val Ala Leu Glu Pro Val Arg Gln Lys Trp
                        135
Gly Leu Asp Arg Ile Ile Val Ser Thr Tyr Gln Ala Val Ser Gly Ala
Gly Met Gly Ala Ile Leu Glu Thr Gln Arg Glu Leu Arg Glu Val Leu
                                    170
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Asn Asp Gly Val Lys Pro Arg Asp Leu His Ala Glu Ile Leu Pro Ser

185

180

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Gly Gly Asp Lys Lys His Tyr Pro Ile Ala Phe Asn Ala Leu Pro Gln
                            200
Ile Asp Val Phe Thr Asp Asn Asp Tyr Thr Tyr Glu Glu Met Lys Met
Thr Lys Glu Thr Lys Lys Ile Met Glu Asp Asp Ser Ile Ala Val Ser
Ala Thr Cys Val Arg Ile Pro Val Leu Ser Ala His Ser Glu Ser Val
                245
Tyr Ile Glu Thr Lys Glu Val Ala Pro Ile Glu Glu Val Lys Ala Ala
                                265
Ile Ala Ala Phe Pro Gly Ala Val Leu Glu Asp Asp Val Ala His Gln
                            280
                                                 285
Ile Tyr Pro Gln Ala Ile Asn Ala Val Gly Ser Arg Asp Thr Phe Val
                        295
Gly Arg Ile Arg Lys Asp Leu Asp Ala Glu Lys Gly Ile His Met Trp
Val Val Ser Asp Asn Leu Leu Lys Gly Ala Ala Trp Asn Ser Val Gln
Ile Ala Glu Thr Leu His Glu Arg Gly Leu Val Arg Pro Thr Ala Glu
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Leu Lys Phe Glu Leu Lys
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<210> 204
<211> 1077
<212> DNA
<213> Streptococcus pneumoniae
<400> 204
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<210> 205

<211> 358

<212> PRT

<213> Streptococcus pneumoniae

<400> 205

Met Gly Tyr Thr Val Ala Val Gly Ala Thr Gly Ala Val Gly Ala 1 5 10 15

Gln Met Ile Lys Met Leu Glu Glu Ser Thr Leu Pro Ile Asp Lys Ile 20 25 30

Arg Tyr Leu Ala Ser Ala Arg Ser Ala Gly Lys Ser Leu Lys Phe Lys 35 40 45

Asp Gln Asp Ile Thr Ile Glu Glu Thr Thr Glu Thr Ala Phe Glu Gly 50 55 60

Val Asp Ile Ala Leu Phe Ser Ala Gly Asp Ser Thr Ser Ala Lys Tyr 65 70 75 80

Ala Pro Tyr Ala Val Lys Ala Gly Val Val Val Val Asp Asn Thr Ser 85 90 95

Tyr Phe Arg Gln Asn Pro Asp Val Pro Leu Val Val Pro Glu Val Asn 100 105 110

Ala His Ala Leu Asp Ala His Asn Gly Ile Ile Ala Cys Pro Asn Cys 115 120 125

Ser Thr Ile Gln Met Met Val Ala Leu Glu Pro Val Arg Gln Lys Trp 130 135 140

Gly Leu Asp Arg Ile Ile Val Ser Thr Tyr Gln Ala Val Ser Gly Ala 145 150 155 160

Gly Met Gly Ala Ile Leu Glu Thr Gln Arg Glu Leu Arg Glu Val Leu 165 170 175

Asn Asp Gly Val Lys Pro Arg Asp Leu His Ala Glu Ile Leu Pro Ser 180 185 190

Gly Gly Asp Lys Lys His Tyr Pro Ile Ala Phe Asn Ala Leu Pro Gln 195 200 205

Ile Asp Val Phe Thr Asp Asn Asp Tyr Thr Tyr Glu Glu Met Lys Met 210 215 220

Thr Lys Glu Thr Lys Lys Ile Met Glu Asp Asp Ser Ile Ala Val Ser 225 230 235 240

Ala Thr Cys Val Arg Ile Pro Val Leu Ser Ala His Ser Glu Ser Val 245 250 255

Tyr	Ile	Glu	Thr 260	Lys	Glu	Val	Ala	Pro 265	Ile	Glu	Glu	Val	Lys 270	Ala	Ala	
Ile	Ala	Ala 275	Phe	Pro	Gly	Ala	Val 280	Leu	Glu	Asp	Asp	Val 285	Ala	His	Gln	
Ile	Tyr 290	Pro	Gln	Ala	Ile	Asn 295	Ala	Val	Gly	Ser	Arg 300	Asp	Thr	Phe	Val	
Gly 305	Arg	Ile	Arg	Lys	Asp 310	Leu	Asp	Ala	Glu	Lys 315	Gly	Ile	His	Met	Trp 320	
Val	Val	Ser	Asp	Asn 325	Leu	Leu	Lys	Gly	Ala 330	Ala	Trp	Asn	Ser	Val 335	Gln	
Ile	Ala	Glu	Thr 340	Leu	His	Glu	Arg	Gly 345	Leu	Val	Arg	Pro	Thr 350	Ala	Glu	
Leu	Lys	Phe 355	Glu	Leu	Lys											
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<211> 34 <212> DNA																
<213> Artificial Sequence																
.220.																
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		cime	_					•		-						
<400 > 206																
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5 5.	, ,,			,,,,				_	_							
-216)> 20	77														
	l> 34															
<212> DNA																
<213	3> A1	rtifi	cia:	l Sec	queno	ce										
<220)>															
<223	3 > De	escri	iptic	oņ of	Art	ific	cial	Sequ	ience	e: Sy	nthe	etic				
	pı	rimer	<u>-</u>													
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gcg	ggat	cc t	ttta	aatto	ca aa	itttc	aatt	cgg	gc .							34
<210)> 20	8														
	L> 62															
	2> PF															
<213	, » » (.reb	.0000	ccus	pnet	HRODI	.ae									
	> 20															
Ser 1	Ile	Ala	Val	Ser	Ala	Thr	Сув	Val		Ile	Pro	Val	Leu		Ala	
_				5					10					15		

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His Ser Glu Ser Val Tyr Ile Glu Thr Lys Glu Val Ala Pro Ile Glu
                                 25
Glu Val Lys Ala Ala Ile Ala Ala Phe Pro Gly Ala Val Leu Glu Asp
Asp Val Ala His Gln Ile Tyr Pro Gln Ala Ile Asn Ala Val
                         55
<210> 209
<211> 19
<212> PRT
<213> Streptococcus pneumoniae
<400> 209
Ser Ala Lys Tyr Ala Pro Tyr Ala Val Lys Ala Gly Val Val Val
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                                     10
Asp Asn Thr
<210> 210
<211> 17
<212> PRT
<213> Streptococcus pneumoniae
<400> 210
Asn Pro Asp Val Pro Leu Val Val Pro Glu Val Asn Ala His Ala Leu
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Asp
<210> 211
<211> 519
<212> DNA
<213> Staphylococcus aureus
<400> 211
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aaggatatta ctacaattat ggataatggt gaagcatatg gctatgcaac agataaaatt 120
gtagaatacg caaaagacag agatgttgat atcgttgtag gacctgaagc gcgtggcttt 180
atcattggct gtcctgtagc ttattcaatg gggattggct ttgcacctgt tagaaaagaa 240
gggaaattac ctcgtgaagt cattcgttat gagtatgacc tagaatatgg tacaaatgtt 300
ttaacaatgc acaaagatgc aattaaacca ggtcaacgtg tgttaattac agatgattta 360
ttagctactg gtggtacgat tgaagcagca ataaaattag ttgaaaaatt aggcggtatc 420
gtagtaggta ttgcatttat aattgaattg aaatatttaa atggtattga aaaaattaaa 480
gattacgatg ttatgagttt aatctcatac gacgaataa
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<210> 212
<211> 172
<212> PRT
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<213> Staphylococcus aureus

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103
<400> 212
Met Asp Leu Lys Gln Tyr Val Ser Glu Val Gln Asp Trp Pro Lys Pro
Gly Val Ser Phe Lys Asp Ile Thr Thr Ile Met Asp Asn Gly Glu Ala
Tyr Gly Tyr Ala Thr Asp Lys Ile Val Glu Tyr Ala Lys Asp Arg Asp
Val Asp Ile Val Val Gly Pro Glu Ala Arg Gly Phe Ile Ile Gly Cys
Pro Val Ala Tyr Ser Met Gly Ile Gly Phe Ala Pro Val Arg Lys Glu
Gly Lys Leu Pro Arg Glu Val Ile Arg Tyr Glu Tyr Asp Leu Glu Tyr
Gly Thr Asn Val Leu Thr Met His Lys Asp Ala Ile Lys Pro Gly Gln
Arg Val Leu Ile Thr Asp Asp Leu Leu Ala Thr Gly Gly Thr Ile Glu
Ala Ala Ile Lys Leu Val Glu Lys Leu Gly Gly Ile Val Val Gly Ile
                        135
Ala Phe Ile Ile Glu Leu Lys Tyr Leu Asn Gly Ile Glu Lys Ile Lys
Asp Tyr Asp Val Met Ser Leu Ile Ser Tyr Asp Glu
                165
<210> 213
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<211> 519

<212> DNA

<213> Staphylococcus aureus

<400> 213

atggatttaa agcaatacgt atcagaagtt caagattggc cgaaaccagg tgttagtttc 60 aaggatatta ctacaattat ggataatggt gaagcatatg gctatgcaac agataaaatt 120 gtagaatacg caaaagacag agatgttgat atcgttgtag gacctgaagc gcgtggcttt 180 atcattggct gtcctgtagc ttattcaatg gggattggct ttgcacctgt tagaaaagaa 240 gggaaattac ctcgtgaagt cattcgttat gagtatgacc tagaatatgg tacaaatgtt 300 ttaaccaatgc acaaagatgc aattaaacca ggtcaacgtg tgttaattac agatgattta 360 ttagctactg gtggtacgat tggaagcag ataaaattag ttgaaaaatt aggcggtatc 420 gtagtaggta ttgcatttat aattgaattg aaatatttaa atggtattga aaaaattaa 480 gattacgatg ttatgagtt taatgagtt taatgagtt taatgagtt 519

<210> 214

<211> 172

<212> PRT

<213> Staphylococcus aureus

Met Asp Leu Lys Gln Tyr Val Ser Glu Val Gln Asp Trp Pro Lys Pro 1 5 10 15

Gly Val Ser Phe Lys Asp Ile Thr Thr Ile Met Asp Asn Gly Glu Ala 20 25 30

Tyr Gly Tyr Ala Thr Asp Lys Ile Val Glu Tyr Ala Lys Asp Arg Asp 40 45

Val Asp Ile Val Val Gly Pro Glu Ala Arg Gly Phe Ile Ile Gly Cys
50 55 60

Pro Val Ala Tyr Ser Met Gly Ile Gly Phe Ala Pro Val Arg Lys Glu 65 70 75 80

Gly Lys Leu Pro Arg Glu Val Ile Arg Tyr Glu Tyr Asp Leu Glu Tyr 85 90 95

Gly Thr Asn Val Leu Thr Met His Lys Asp Ala Ile Lys Pro Gly Gln
100 105 110

Arg Val Leu Ile Thr Asp Asp Leu Leu Ala Thr Gly Gly Thr Ile Glu
115 120 125

Ala Ala Ile Lys Leu Val Glu Lys Leu Gly Gly Ile Val Val Gly Ile 130 135 140

Ala Phe Ile Ile Glu Leu Lys Tyr Leu Asn Gly Ile Glu Lys Ile Lys 145 150 155 160

Asp Tyr Asp Val Met Ser Leu Ile Ser Tyr Asp Glu 165 170

<210> 215

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 215

gcggcggcat taatatggat ttaaagcaat acgtatc

37

<210> 216

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

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<400> 216
                                                                   32
gegeggatee ttegtegtat gagattaaac te
<210> 217
<211> 11
<212> PRT
<213> Staphylococcus aureus
<400> 217
Gly Phe Ile Ile Gly Cys Pro Val Ala Tyr Ser
<210> 218
<211> 7
<212> PRT
<213> Staphylococcus aureus
<400> 218
Val Asp Ile Val Val Gly Pro
<210> 219
<211> 26
<212> PRT
<213> Staphylococcus aureus
<400> 219
Glu Ala Ala Ile Lys Leu Val Glu Lys Leu Gly Gly Ile Val Val Gly
Ile Ala Phe Ile Ile Glu Leu Lys Tyr Leu
<210> 220
<211> 777
<212> DNA
<213> Staphylococcus aureus
<400> 220
gtgtcttctt tacttgtata tgttacatat attcacgata gagaggataa gaaaatggct 60
caaatttcta aatataaacg tgtagttttg aaactaagtg gtgaagcgtt agctggagaa 120
aaaggatttg gcataaatcc agtaattatt aaaagtgttg ctgagcaagt ggctgaagtt 180
gctaaaatgg actgtgaaat cgcagtaatc gttggtggcg gaaacatttg gagaggtaaa 240
acaggtagtg acttaggtat ggaccgtgga actgctgatt acatgggtat gcttgcaact 300
gtaatgaatg ccttagcatt acaagatagt ttagaacaat tggattgtga tacacgagta 360
ttaacatcta ttgaaatgaa gcaagtggct gaaccttata ttcgtcgtcg tgcaattaga 420
cacttagaaa agaaacgcgt agttattttt gctgcaggta ttggaaaccc atacttctct 480
acagatacta cagcggcatt acgtgctgca gaagttgaag cagatgttat tttaatgggc 540
aaaaataatg tagatggtgt atattctgca gatcctaaag taaacaaaga tgcggtaaaa 600
tatgaacatt taacgcatat tcaaatgctt caagaaggtt tacaagtaat ggattcaaca 660
gcatcctcat tctgtatgga taataacatt ccgttaactg ttttctctat tatggaagaa 720
ggaaatatta aacgtgctgt tatgggtgaa aagataggta cgttaattac aaaataa 777
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- <210> 221
- <211> 258
- <212> PRT
- <213> Staphylococcus aureus

- Val Ser Ser Leu Leu Val Tyr Val Thr Tyr Ile His Asp Arg Glu Asp 1 5 10 15
- Lys Lys Met Ala Gln Ile Ser Lys Tyr Lys Arg Val Val Leu Lys Leu 20 25 30
- Ser Gly Glu Ala Leu Ala Gly Glu Lys Gly Phe Gly Ile Asn Pro Val\$35\$ 40 45
- Ile Ile Lys Ser Val Ala Glu Gln Val Ala Glu Val Ala Lys Met Asp 50 55 60
- Cys Glu Ile Ala Val Ile Val Gly Gly Gly Asn Ile Trp Arg Gly Lys
 65 70 75 80
- Thr Gly Ser Asp Leu Gly Met Asp Arg Gly Thr Ala Asp Tyr Met Gly 85 90 95
- Met Leu Ala Thr Val Met Asn Ala Leu Ala Leu Gln Asp Ser Leu Glu
 100 105 110
- Gln Leu Asp Cys Asp Thr Arg Val Leu Thr Ser Ile Glu Met Lys Gln 115 120 125
- Val Ala Glu Pro Tyr Ile Arg Arg Ala Ile Arg His Leu Glu Lys 130 135 140
- Lys Arg Val Val Ile Phe Ala Ala Gly Ile Gly Asn Pro Tyr Phe Ser 145 150 155 160
- Thr Asp Thr Thr Ala Ala Leu Arg Ala Ala Glu Val Glu Ala Asp Val
 165 170 175
- Ile Leu Met Gly Lys Asn Asn Val Asp Gly Val Tyr Ser Ala Asp Pro 180 185 190
- Lys Val Asn Lys Asp Ala Val Lys Tyr Glu His Leu Thr His Ile Gln 195 200 205
- Met Leu Gln Glu Gly Leu Gln Val Met Asp Ser Thr Ala Ser Ser Phe 210 215 220
- Cys Met Asp Asn Asn Ile Pro Leu Thr Val Phe Ser Ile Met Glu Glu 225 230 235 240
- Gly Asn Ile Lys Arg Ala Val Met Gly Glu Lys Ile Gly Thr Leu Ile 245 250 255

Thr Lys

<210> 222

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<211> 777
<212> DNA
<213> Staphylococcus aureus
<400> 222
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caaatttcta aatataaacg tgtagttttg aaactaagtg gtgaagcgtt agctggagaa 120
aaaggatttg gcataaatcc agtaattatt aaaagtgttg ctgagcaagt ggctgaagtt 180
gctaaaatgg actgtgaaat cgcagtaatc gttggtggcg gaaacatttg gagaggtaaa 240
ccaggtagtg acttaggtat ggaccgtgga actgctgatt acatgggtat gcttgcaact 300
gtaatgaatg etttageatt acaagatagt ttagaacaat tggattgtga tacaegagta 360
ttaacatcta ttgaaatgaa gcaagtggct gaaccttata ttcgtcgtcg tgcaattaga 420
cacttagaaa agaaacgcgt agttattttt gctgcaggta ttggaaaccc atacttctct 480
acagatacta cagcggcatt acgtgctgca gaagttgaag cagatgttat tttaatgggc 540
aaaaataatg tagatggtgt atattetgea gateetaaag taaacaaaga tgeggtaaaa 600
tatgaacatt taacgcatat tcaaatgctt caagaaggtt tacaagtaat ggattcaaca 660
gcatcctcat tctgtatgga taataacatt ccgttaactg ttttctctat tatggaagaa 720
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<210> 223
<211> 258
<212> PRT
<213> Staphylococcus aureus
<400> 223
Val Ser Ser Leu Leu Val Tyr Val Thr Tyr Ile His Asp Arg Glu Asp
                                     10
Lys Lys Met Ala Gln Ile Ser Lys Tyr Lys Arg Val Val Leu Lys Leu
Ser Gly Glu Ala Leu Ala Gly Glu Lys Gly Phe Gly Ile Asn Pro Val
Ile Ile Lys Ser Val Ala Glu Gln Val Ala Glu Val Ala Lys Met Asp
Cys Glu Ile Ala Val Ile Val Gly Gly Gly Asn Ile Trp Arg Gly Lys
Pro Gly Ser Asp Leu Gly Met Asp Arg Gly Thr Ala Asp Tyr Met Gly
Met Leu Ala Thr Val Met Asn Ala Leu Ala Leu Gln Asp Ser Leu Glu
Gln Leu Asp Cys Asp Thr Arg Val Leu Thr Ser Ile Glu Met Lys Gln
        115
                            120
Val Ala Glu Pro Tyr Ile Arg Arg Ala Ile Arg His Leu Glu Lys
Lys Arg Val Val Ile Phe Ala Ala Gly Ile Gly Asn Pro Tyr Phe Ser
                                        155
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Thr Asp Thr Thr Ala Ala Leu Arg Ala Ala Glu Val Glu Ala Asp Val

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Ile Leu Met Gly Lys Asn Asn Val Asp Gly Val Tyr Ser Ala Asp Pro
Lys Val Asn Lys Asp Ala Val Lys Tyr Glu His Leu Thr His Ile Gln
        195
                             200
Met Leu Gln Glu Gly Leu Gln Val Met Asp Ser Thr Ala Ser Ser Phe
                         215
Cys Met Asp Asn Asn Ile Pro Leu Thr Val Phe Ser Ile Met Glu Glu
225
                                         235
Gly Asn Ile Lys Arg Ala Val Met Gly Glu Lys Ile Gly Thr Leu Ile
                                     250
Thr Lys
<210> 224
<211> 38
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 224
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                                                                    38
<210> 225
<211> 37
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 225
gcgcggatcc ttttgtaatt aacgtaccta tcttttc
                                                                    37
<210> 226
<211> 8
<212> PRT
<213> Staphylococcus aureus
<400> 226
Leu Leu Val Tyr Val Thr Tyr Ile
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i

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<210> 227
<211> 12
<212> PRT
<213> Staphylococcus aureus
<400> 227
Lys Met Asp Cys Glu Ile Ala Val Ile Val Gly Gly
                 5
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<210> 228
<211> 14
<212> PRT
<213> Staphylococcus aureus
<400> 228
Ile Ser Lys Tyr Lys Arg Val Val Leu Lys Leu Ser Gly Glu
<210> 229
<211> 627
<212> DNA
<213> Streptococcus pneumoniae
<400> 229
atggcagacc gaggcttact aatcgttttt tctggtcctt caggggttgg aaaaggaacg 60
gttagaagag agatttttga gagttctgaa aaccaatttc aatattctgt atcgatgacg 120
acacgcgcac aacgtcctgg agaagtggac ggtgttgact atttcttccg tactcgtgaa 180
gaatttgaag agctgattcg tcaaggacag atgttggaat acgcagaata tgtcggtaac 240
tactatggaa ctcctctgac ctatgtcaat gaaaccttgg acaagggaat cgatgttttc 300
cttgaaattg aagttcaggg tgctcttcag gtcaagaaaa aggttccaga tgctgtcttt 360
atcttcctga caccaccaga tttggatgaa ttgcaagatc gcttggtagg tcgtggaaca 420
gatagtgcag aagtgattgc ccaacgaatc gaaaaggcca aggaagaaat tgccctcatg 480
cgtgagtatg attatgcgat tgtcaacgat caggtacccc tagctgctga acgtgtcaaa 540
tgtgtgattg aagcagaaca cttctgtgtg gatcgtgtca ttggtcacta tcaggagatg 600
ttaccaaaat ctccaactac ccgataa
<210> 230
<211> 208
<212> PRT
<213> Streptococcus pneumoniae
<400> 230
Met Ala Asp Arg Gly Leu Leu Ile Val Phe Ser Gly Pro Ser Gly Val
Gly Lys Gly Thr Val Arg Arg Glu Ile Phe Glu Ser Ser Glu Asn Gln
             20
                                 25
Phe Gln Tyr Ser Val Ser Met Thr Thr Arg Ala Gln Arg Pro Gly Glu
Val Asp Gly Val Asp Tyr Phe Phe Arg Thr Arg Glu Glu Phe Glu Glu
            、 55
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Leu Ile Arg Gln Gly Gln Met Leu Glu Tyr Ala Glu Tyr Val Gly Asn
                     70
Tyr Tyr Gly Thr Pro Leu Thr Tyr Val Asn Glu Thr Leu Asp Lys Gly
Ile Asp Val Phe Leu Glu Ile Glu Val Gln Gly Ala Leu Gln Val Lys
            100
                                105
Lys Lys Val Pro Asp Ala Val Phe Ile Phe Leu Thr Pro Pro Asp Leu
Asp Glu Leu Gln Asp Arg Leu Val Gly Arg Gly Thr Asp Ser Ala Glu
    130
Val Ile Ala Gln Arg Ile Glu Lys Ala Lys Glu Glu Ile Ala Leu Met
Arg Glu Tyr Asp Tyr Ala Ile Val Asn Asp Gln Val Pro Leu Ala Ala
                165
                                    170
Glu Arg Val Lys Cys Val Ile Glu Ala Glu His Phe Cys Val Asp Arg
Val Ile Gly His Tyr Gln Glu Met Leu Pro Lys Ser Pro Thr Thr Arg
                            200
<210> 231
<211> 627
<212> DNA
<213> Streptococcus pneumoniae
<400> 231
atggcagacc gaggcttact aatcgttttt tctggtcctt caggggttgg aaaaggaacg 60
gttagaagag agatttttga gagttctgaa aaccaatttc aatactctgt atcgatgacg 120
acacgcgcac aacgtcctgg agaagtggac ggtgttgact atttcttccg tactcgtgaa 180
gaatttgaag agctgattcg tcaaggacag atgttggaat acgcagaata tgtcggcaac 240
tactatggaa ctcctctgac ctatgtcaat gaaaccttgg acaagggaat cgatgttttc 300
cttgaaattg aagttcaggg tgctcttcag gtcaagaaaa aggttccaga tgctgtcttt 360
atetteetga caccaccaga tttggatgaa ttgcaagate gettggtagg tegtggaaca 420
gatagtgcag aagtgattgc ccaacgaatc gaaaaggcca aggaagaaat tgccctcatg 480
cgtgagtatg attatgcgat tgtcaacgat caggtacccc tagctgctga acgtgtcaaa 540
tgtgtgattg aagcagaaca cttctgtgtg gatcgtgtca ttggtcacta tcaggagatg 600
ttaccaaaat ctccaactac ccgataa
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<210> 232

<211> 208

<212> PRT

<213> Streptococcus pneumoniae

<400> 232

Met Ala Asp Arg Gly Leu Leu Ile Val Phe Ser Gly Pro Ser Gly Val

1 10 15

. Gly Lys Gly Thr Val Arg Arg Glu Ile Phe Glu Ser Ser Glu Asn Gln
20 25 30

Phe Gln Tyr Ser Val Ser Met Thr Thr Arg Ala Gln Arg Pro Gly Glu 35 40 45

Val Asp Gly Val Asp Tyr Phe Phe Arg Thr Arg Glu Glu Phe Glu Glu 50 55 60

Leu Ile Arg Gln Gly Gln Met Leu Glu Tyr Ala Glu Tyr Val Gly Asn 65 70 75 80

Tyr Tyr Gly Thr Pro Leu Thr Tyr Val Asn Glu Thr Leu Asp Lys Gly 85 90 95

Ile Asp Val Phe Leu Glu Ile Glu Val Gln Gly Ala Leu Gln Val Lys
100 105 110

Lys Lys Val Pro Asp Ala Val Phe Ile Phe Leu Thr Pro Pro Asp Leu 115 120 125

Asp Glu Leu Gln Asp Arg Leu Val Gly Arg Gly Thr Asp Ser Ala Glu 130 135 140

Arg Glu Tyr Asp Tyr Ala Ile Val Asn Asp Gln Val Pro Leu Ala Ala 165 170 175

Glu Arg Val Lys Cys Val Ile Glu Ala Glu His Phe Cys Val Asp Arg 180 185 190

Val Ile Gly His Tyr Gln Glu Met Leu Pro Lys Ser Pro Thr Thr Arg 195 200 205

<210> 233

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 233

gcggcggccc atatggcaga ccgaggctta c

31

<210> 234

<211> 30

<212> DNA

<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 234
gcgcggatcc tcgggtagtt ggagattttg
                                                                   30
<210> 235
<211> 33
<212> PRT
<213> Streptococcus pneumoniae
<400> 235
Asp Tyr Ala Ile Val Asn Asp Gln Val Pro Leu Ala Ala Glu Arg Val
Lys Cys Val Ile Glu Ala Glu His Phe Cys Val Asp Arg Val Ile Gly
                                 25
His
<210> 236
<211> 13
<212> PRT
<213> Streptococcus pneumoniae
<400> 236
Arg Gly Leu Leu Ile Val Phe Ser Gly Pro Ser Gly Val
<210> 237
<211> 31
<212> PRT
<213> Streptococcus pneumoniae
<400> 237
Gly Ile Asp Val Phe Leu Glu Ile Glu Val Gln Gly Ala Leu Gln Val
Lys Lys Lys Val Pro Asp Ala Val Phe Ile Phe Leu Thr Pro Pro
<210> 238
<211> 513
<212> DNA
<213> Streptococcus pneumoniae
<400> 238
atgaatttaa aagattacat tgcaacaatt gaaaattatc caaaggaagg cattaccttc 60
cgtgatatta gtcctttgat ggctgatgga aatgcttata gctacgctgt tcgtgaaatc 120
gttcagtatg ctactgacaa gaaagtcgac atgatcgtgg gacctgaagc tcgtggattt 180
atcgtgggtt gtccagttgc ctttgagttg ggaattggtt ttgcgcctgt tcgtaagcca 240
ggtaaattgc cacgcgaagt tatttctgct gactatgaaa aagagtacgg tgtcgatacc 300
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ttgactatgc acgcggatgc cattaagcca ggtcaacgtg ttcttattgt agatgacctt 360 ttggcgacag gtggaactgt taaggcaact atcgagatga ttgaaaaact tggtggtgtt 420

atggcaggtt gtgccttcct tgttgaattg gatgaattga acggccgtga aaaaattggt 480 gactacgact acaaagttct tatgcattat taa <210> 239 <211> 170 <212> PRT <213> Streptococcus pneumoniae <400> 239 Met Asn Leu Lys Asp Tyr Ile Ala Thr Ile Glu Asn Tyr Pro Lys Glu Gly Ile Thr Phe Arg Asp Ile Ser Pro Leu Met Ala Asp Gly Asn Ala 25 Tyr Ser Tyr Ala Val Arg Glu Ile Val Gln Tyr Ala Thr Asp Lys Lys 40 Val Asp Met Ile Val Gly Pro Glu Ala Arg Gly Phe Ile Val Gly Cys Pro Val Ala Phe Glu Leu Gly Ile Gly Phe Ala Pro Val Arg Lys Pro Gly Lys Leu Pro Arg Glu Val Ile Ser Ala Asp Tyr Glu Lys Glu Tyr 85 Gly Val Asp Thr Leu Thr Met His Ala Asp Ala Ile Lys Pro Gly Gln 105 Arg Val Leu Ile Val Asp Asp Leu Leu Ala Thr Gly Gly Thr Val Lys Ala Thr Ile Glu Met Ile Glu Lys Leu Gly Gly Val Met Ala Gly Cys 135 Ala Phe Leu Val Glu Leu Asp Glu Leu Asn Gly Arg Glu Lys Ile Gly 145 150 155 160 Asp Tyr Asp Tyr Lys Val Leu Met His Tyr 165 <210> 240 <211> 513 <212> DNA <213> Streptococcus pneumoniae <400> 240 atgaatttaa aagattacat tgcaacaatt gaaaattatc caaaggaagg cattaccttc 60 cgtgatatta gtcctttgat ggctgatgga aatgcttata gctacgctgt tcgtgaaatc 120 gttcagtatg ctactgacaa gaaagtcgac atgatcgtgg gacctgaagc tcgtggattt 180 atcgtgggtt gtccagttgc ctttgagttg ggaattggtt ttgcgcctgt tcgtaagcca 240 ggtaaattgc cacgcgaagt tatttctgct gactatgaaa aagagtacgg tgtcgatact 300

ttgactatgc acgcggatgc cattaagcca ggtcaacgtg ttcttattgt agatgacctt 360

ttggcgacag gtggaactgt taaggcaact atcgagatga ttgaaaaact tggtggtgtt 420 atggcaggtt gtgccttcct tgttgaattg gatgaattga acggccgtga aaaaattggt 480 gactacgact acaaagttct tatgcattat taa 513

<210> 241

<211> 170

<212> PRT

<213> Streptococcus pneumoniae

<400> 241

Met Asn Leu Lys Asp Tyr Ile Ala Thr Ile Glu Asn Tyr Pro Lys Glu
1 5 10 15

Gly Ile Thr Phe Arg Asp Ile Ser Pro Leu Met Ala Asp Gly Asn Ala 20 25 30

Tyr Ser Tyr Ala Val Arg Glu Ile Val Gln Tyr Ala Thr Asp Lys Lys
35 40 45

Val Asp Met Ile Val Gly Pro Glu Ala Arg Gly Phe Ile Val Gly Cys
50 55 60

Pro Val Ala Phe Glu Leu Gly Ile Gly Phe Ala Pro Val Arg Lys Pro 65 70 75 80

Gly Lys Leu Pro Arg Glu Val Ile Ser Ala Asp Tyr Glu Lys Glu Tyr 85 90 95

Gly Val Asp Thr Leu Thr Met His Ala Asp Ala Ile Lys Pro Gly Gln
100 105 110

Arg Val Leu Ile Val Asp Asp Leu Leu Ala Thr Gly Gly Thr Val Lys
115 120 125

Ala Thr Ile Glu Met Ile Glu Lys Leu Gly Gly Val Met Ala Gly Cys

Ala Phe Leu Val Glu Leu Asp Glu Leu Asp Gly Arg Glu Lys Ile Gly 145 150 155 160

Asp Tyr Asp Tyr Lys Val Leu Met His Tyr 165 170

<210> 242

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 242

gcggcggccc atatgaattt aaaagattac attgcaac

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<210> 243
<211> 34
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 243
                                                                   34
gcgcggatcc ataatgcata agaactttgt agtc
<210> 244
<211> 22
<212> PRT
<213> Streptococcus pneumoniae
<400> 244
Gly Phe Ile Val Gly Cys Pro Val Ala Phe Glu Leu Gly Ile Gly Phe
Ala Pro Val Arg Lys Pro
<210> 245
<211> 13
<212> PRT
<213> Streptococcus pneumoniae
<400> 245
Gly Val Met Ala Gly Cys Ala Phe Leu Val Glu Leu Asp
<210> 246
<211> 14
<212> PRT
<213> Streptococcus pneumoniae
<400> 246
Gly Gln Arg Val Leu Ile Val Asp Asp Leu Leu Ala Thr Gly
<210> 247
<211> 744
<212> DNA
<213> Streptococcus pneumoniae
<400> 247
gtgaaaatgg cgaatcccaa gtataaacgt attttaatca agttatcagg tgaagccctt 60
gccggtgaac gtggcgtagg gattgatatc caaacagttc aaacaatcgc aaaagagatt 120
caagaagttc atagcttagg tatcgaaatt gcccttgtta tcggtggagg aaatctctgg 180
cgtggagaac ctgcagcaga agcaggtatg gaccgtgttc aggcagatta cacaggaatg 240
cttgggactg ttatgaatgc tcttgtgatg gcagattcat tgcaacaagt tggggttgat 300
acgcgtgtac aaacagctat tgccatgcaa caagtggcag agccttatgt ccgtggacgt 360
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gcccttcgtc accttgaaaa aggccgtatc gttatctttg gtgctggaat tggttcacct 420 tacttctcga cagatacaac agcggcctt cgtgcagctg aaatcgaagc agatgccatc 480 ctcatggcta aaaatggtgt cgatggtgtt tacaatgccg atcctaagaa agataagaca 540 gctgttaagt ttgaagaatt gacccaccgt gacgttatca ataaaggtct tcgtatcatg 600 gactcaacag cttcaaccct ctcaatggac aacgacattg acttggtgt attcaacatg 660 aaccaaccag gcaacatcaa acgtgtcgta tttggtgaaa ataatcggaac aacagtttca 720 aataatatcg aagaaaagga ataa

<210> 248

<211> 247

<212> PRT

<213> Streptococcus pneumoniae

<400> 248

Val Lys Met Ala Asn Pro Lys Tyr Lys Arg Ile Leu Ile Lys Leu Ser 1 5 10 15

Gly Glu Ala Leu Ala Gly Glu Arg Gly Val Gly Ile Asp Ile Gln Thr 20 25 30

Val Gln Thr Ile Ala Lys Glu Ile Gln Glu Val His Ser Leu Gly Ile 35 40 45

Glu Ile Ala Leu Val Ile Gly Gly Gly Asn Leu Trp Arg Gly Glu Pro
50 55 60

Ala Ala Glu Ala Gly Met Asp Arg Val Gln Ala Asp Tyr Thr Gly Met 65 70 75 80

Leu Gly Thr Val Met Asn Ala Leu Val Met Ala Asp Ser Leu Gln Gln 85 90 95

Val Gly Val Asp Thr Arg Val Gln Thr Ala Ile Ala Met Gln Gln Val 100 105 110

Ala Glu Pro Tyr Val Arg Gly Arg Ala Leu Arg His Leu Glu Lys Gly
115 120 125

Arg Ile Val Ile Phe Gly Ala Gly Ile Gly Ser Pro Tyr Phe Ser Thr 130 135 140

Asp Thr Thr Ala Ala Leu Arg Ala Ala Glu Ile Glu Ala Asp Ala Ile 145 150 155 160

Leu Met Ala Lys Asn Gly Val Asp Gly Val Tyr Asn Ala Asp Pro Lys 165 170 175

Lys Asp Lys Thr Ala Val Lys Phe Glu Glu Leu Thr His Arg Asp Val

Ile Asn Lys Gly Leu Arg Ile Met Asp Ser Thr Ala Ser Thr Leu Ser 195 200 205

Met Asp Asn Asp Ile Asp Leu Val Val Phe Asn Met Asn Gln Pro Gly 210 215 220

Asn Ile Lys Arg Val Val Phe Gly Glu Asn Ile Gly Thr Thr Val Ser 225 Asn Asn Ile Glu Glu Lys Glu 245 <210> 249 <211> 744 <212> DNA <213> Streptococcus pneumoniae <400> 249 gtgaaaatgg cgaatcccaa gtataaacgt attttaatca agttatcagg tgaagccctt 60 gccggtgaac gtggcgtagg gattgatatc caaacagttc aaacaatcgc aaaagagatt 120 caagaagttc atagcttagg tatcgaaatt gcccttgtta ttggtggagg aaatctctgg 180 cgtggagacc ctgcagcaga agcaggtatg gaccgtgttc aggcagatta cactggaatg 240 cttgggactg ttatgaatgc tcttgtgatg gcagattcat tgcaacaagt tggggttgat 300 acgcgtgtac aaacagctat tgctatgcaa caagtggcag agccttatgt ccgtggacgt 360 gcccttcgtc accttgaaaa aggccgtatc gttatctttg gtgctggaat tggttcacca 420 tacttctcga cagatacaac agcggccctt cgtgcagctg aaatcgaagc agatgccatc 480 ctcatggcta aaaatggcgt cgatggtgtg tacaatgccg atcctaagaa ggacaagaca 540 gccgttaagt ttgaagaatt gacccaccgt gatgttatca acaaaggtct tcgtatcatg 600 gactcaacag cctcaaccct ctcaatggac aacgacattg acttggttgt cttcaacatg 660 aaccaatcag gcaacatcaa acgtgtcgta tttggtgaaa atatcggaac aacagtttca 720 aataatatcg aagaaaagga ataa <210> 250 <211> 247 <212> PRT <213> Streptococcus pneumoniae <400> 250 Val Lys Met Ala Asn Pro Lys Tyr Lys Arg Ile Leu Ile Lys Leu Ser Gly Glu Ala Leu Ala Gly Glu Arg Gly Val Gly Ile Asp Ile Gln Thr 20 Val Gln Thr Ile Ala Lys Glu Ile Gln Glu Val His Ser Leu Gly Ile Glu Ile Ala Leu Val Ile Gly Gly Asn Leu Trp Arg Gly Asp Pro Ala Ala Glu Ala Gly Met Asp Arg Val Gln Ala Asp Tyr Thr Gly Met 70 Leu Gly Thr Val Met Asn Ala Leu Val Met Ala Asp Ser Leu Gln Gln Val Gly Val Asp Thr Arg Val Gln Thr Ala Ile Ala Met Gln Gln Val

Ala Glu Pro Tyr Val Arg Gly Arg Ala Leu Arg His Leu Glu Lys Gly

Arg Ile Val Ile Phe Gly Ala Gly Ile Gly Ser Pro Tyr Phe Ser Thr Asp Thr Thr Ala Ala Leu Arg Ala Ala Glu Ile Glu Ala Asp Ala Ile Leu Met Ala Lys Asn Gly Val Asp Gly Val Tyr Asn Ala Asp Pro Lys 165 170 Lys Asp Lys Thr Ala Val Lys Phe Glu Glu Leu Thr His Arg Asp Val Ile Asn Lys Gly Leu Arg Ile Met Asp Ser Thr Ala Ser Thr Leu Ser Met Asp Asn Asp Ile Asp Leu Val Val Phe Asn Met Asn Gln Ser Gly Asn Ile Lys Arg Val Val Phe Gly Glu Asn Ile Gly Thr Thr Val Ser 230 235 240 Asn Asn Ile Glu Glu Lys Glu 245 <210> 251 <211> 33 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic primer <400> 251 gcggcggccc atatgaaaat ggcgaatccc aag 33 <210> 252 <211> 33 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic primer <400> 252 gcgcggatcc ttccttttct tcgatattat ttg 33 <210> 253 <211> 33 <212> DNA

<213> Artificial Sequence

<220> <223>	Description of Artificial Sequence: Synthetic primer	
<400> gcggc	253 ggccc atatgaaaat ggcgaatccc aag	33
<210><211><211><212><213>	34	
<220> <223>	Description of Artificial Sequence: Synthetic primer	
<400> gcggcg	254 ggccc atatggcgaa tcccaagtat aaac	34
<210><211><211><212><213>	42	
<220> <223>	Description of Artificial Sequence: Synthetic primer	
<400> 255 gcggcggccc atatgaatcc caagtataaa cgtattttaa tc		42
	36	
<220> <223>	Description of Artificial Sequence: Synthetic primer	
<400> gcggcg	256 ggccc atatgaagta taaacgtatt ttaatc	36
<210><211><211><212><213>	38	
<220> <223>	Description of Artificial Sequence: Synthetic primer	
<400> gcggcg	257 ggccc atatgaaacg tattttaatc aagttatc	38

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<210> 258
<211> 35
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      primer
                                                                    35
gcggcggccc atatgatttt aatcaagtta tcagg
<210> 259
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
<400> 259
                                                                    33
gcggcggccc atatgaagtt atcaggtgaa gcc
<210> 260
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 260
                                                                    33
gcgcggatcc ttccttttct tcgatattat ttg
<210> 261
<211> 34
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 261
gcgcggatcc tgttccgata ttttcaccaa atac
                                                                    34
<210> 262
<211> 33
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 262
gcgcggatcc aactgttgtt ccgatatttt cac
                                                                    33
<210> 263
<211> 37
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
<400> 263
gcgcggatcc atttgaaact gttgttccga tattttc
                                                                    37
<210> 264
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 264
gcgcggatcc gatattattt gaaactgttg ttc
                                                                    33
<210> 265
<211> 31
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 265
gcgcggatcc attttcacca aatacgacac g
                                                                    31
<210> 266
<211> 30
<212> PRT
<213> Streptococcus pneumoniae
<400> 266
Gly Ile Asp Ile Gln Thr Val Gln Thr Ile Ala Lys Glu Ile Gln Glu
                                      10
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Val His Ser Leu Gly Ile Glu Ile Ala Leu Val Ile Gly Gly
             20
                                 25
<210> 267
<211> 7
<212> PRT
<213> Streptococcus pneumoniae
<400> 267
Ile Asp Leu Val Val Phe Asn
 1
                  5
<210> 268
<211> 37
<212> PRT
<213> Streptococcus pneumoniae
<400> 268
Val Met Asn Ala Leu Val Met Ala Asp Ser Leu Gln Gln Val Gly Val
Asp Thr Arg Val Gln Thr Ala Ile Ala Met Gln Gln Val Ala Glu Pro
                                 25
Tyr Val Arg Gly Arg
         35
<210> 269
<211> 738
<212> DNA
<213> Pseudomonas aeruginosa
<400> 269
atggeteage aactgagege tegteaacet egetataaac geattettet aaagttgage 60
ggcgaagccc tgatgggctc ggaggagttc ggcattgatc ccaaggtgct ggaccgcatg 120
gcgctggaaa tcggccagtt ggtcgggatc ggcgtgcagg tcggcctggt catcggcggc 180
ggcaacctgt teegeggege ggceetgtee geggeeggea tggaeegggt gaeeggegae 240
cacatgggga tgctggccac cgtgatgaac ggcctggcga tgcgcgatgc gctggagcgc 300
tcgaacatcc ccgcgctggt gatgtcggcg atctccatgg tcggtgtgac cgaccactac 360
gaccgccgca aggccatgcg ccacctcggc ggtggcgagg tggtgatctt ctccgccggt 420
accggcaacc cgttcttcac caccgactcg gcggcttgcc tgcgcgccat cgagatcgac 480
gccgacgtgg tccttaaggc taccaaggtc gatggcgtgt acactgccga cccgttcaag 540
gacccgaatg ccgagaagtt cgagcgcctg acctatgatg aagtgctcga ccgcaagctc 600
ggcgtgatgg acctgaccgc catctgcctg tgccgtgacc agaacatgcc gctgcgggtg 660
ttcaacatga acaagccggg cgcattgctg aatattgttg ttggtggtgc cgaaggcacc 720
ctgatcgagg agggttga
                                                                   738
```

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<210> 270
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<211> 245

<212> PRT

<213> Pseudomonas aeruginosa

<400> 270

Met Ala Gln Gln Leu Ser Ala Arg Gln Pro Arg Tyr Lys Arg Ile Leu 1 5 10 15

Leu Lys Leu Ser Gly Glu Ala Leu Met Gly Ser Glu Glu Phe Gly Ile 20 25 30

Asp Pro Lys Val Leu Asp Arg Met Ala Leu Glu Ile Gly Gln Leu Val
35 40 45

Gly Ile Gly Val Gln Val Gly Leu Val Ile Gly Gly Asn Leu Phe 50 55 60

Arg Gly Ala Ala Leu Ser Ala Ala Gly Met Asp Arg Val Thr Gly Asp 65 70 75 80

His Met Gly Met Leu Ala Thr Val Met Asn Gly Leu Ala Met Arg Asp 85 90 95

Ala Leu Glu Arg Ser Asn Ile Pro Ala Leu Val Met Ser Ala Ile Ser 100 105 110

Met Val Gly Val Thr Asp His Tyr Asp Arg Arg Lys Ala Met Arg His 115 120 125

Leu Gly Gly Glu Val Val Ile Phe Ser Ala Gly Thr Gly Asn Pro 130 135 140

Phe Phe Thr Thr Asp Ser Ala Ala Cys Leu Arg Ala Ile Glu Ile Asp 145 150 155 160

Ala Asp Val Val Leu Lys Ala Thr Lys Val Asp Gly Val Tyr Thr Ala 165 170 175

Asp Pro Phe Lys Asp Pro Asn Ala Glu Lys Phe Glu Arg Leu Thr Tyr 180 185 190

Asp Glu Val Leu Asp Arg Lys Leu Gly Val Met Asp Leu Thr Ala Ile 195 200 205

Cys Leu Cys Arg Asp Gln Asn Met Pro Leu Arg Val Phe Asn Met Asn 210 215 220

Lys Pro Gly Ala Leu Leu Asn Ile Val Val Gly Gly Ala Glu Gly Thr 225 230 235 240

Leu Ile Glu Glu Gly

<210> 271

<211> 738

<212> DNA

<213> Pseudomonas aeruginosa

<400> 271

atggctcagc aactgagcgc tcgtcaacct cgctataaac gcattcttct aaagttgagc 60 ggcgaagccc tgatgggctc ggaggagttc ggcatcgatc ccaaggtgct ggaccgcatg 120

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gegetggaaa teggeeagtt ggtegggate ggegtgeagg teggeetggt categgegge 180
ggcaacctgt teegeggege ggeeetgtee geggeeggea tggaeegggt gaeeggegae 240
cacatgggga tgctggccac cgtgatgaac ggcctggcga tgcgcgatgc gctggagcgc 300
tegaacatee eegegetggt gatgteggeg atetecatgg teggtgtgae egaceactae 360
gaccgccgca aggccatgcg ccacctcggc ggtggcgagg tggtgatctt ctccgccggt 420
accggcaacc cgttcttcac caccgactcg gcggcttgcc tgcgcgccat cgagatcgac 480
gccgacgtgg tccttaaggc taccaaggtc gatggcgtgt acactgccga cccgttcaag 540
gacccgaatg ccgagaagtt cgagcgcctg acctatgatg aagtgctcga ccgcaagctc 600
ggcgtgatgg acctgaccgc catctgcctg tgccgtgacc agaacatgcc gctgcgggtg 660
ttcaacatga acaagccggg cgcattgctg aatattgttg ttggtggtgc cgaaggcacc 720
ctgatcgagg agggttga
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<210> 272

<211> 245

<212> PRT

<213> Pseudomonas aeruginosa

<400> 272

Met Ala Gln Gln Leu Ser Ala Arg Gln Pro Arg Tyr Lys Arg Ile Leu

Leu Lys Leu Ser Gly Glu Ala Leu Met Gly Ser Glu Glu Phe Gly Ile

Asp Pro Lys Val Leu Asp Arg Met Ala Leu Glu Ile Gly Gln Leu Val 35

Gly Ile Gly Val Gln Val Gly Leu Val Ile Gly Gly Gly Asn Leu Phe

Arg Gly Ala Ala Leu Ser Ala Ala Gly Met Asp Arg Val Thr Gly Asp 70

His Met Gly Met Leu Ala Thr Val Met Asn Gly Leu Ala Met Arg Asp

Ala Leu Glu Arg Ser Asn Ile Pro Ala Leu Val Met Ser Ala Ile Ser 100 105

Met Val Gly Val Thr Asp His Tyr Asp Arg Arg Lys Ala Met Arg His

Leu Gly Gly Glu Val Val Ile Phe Ser Ala Gly Thr Gly Asn Pro

Phe Phe Thr Thr Asp Ser Ala Ala Cys Leu Arg Ala Ile Glu Ile Asp 145 150

Ala Asp Val Val Leu Lys Ala Thr Lys Val Asp Gly Val Tyr Thr Ala 170

Asp Pro Phe Lys Asp Pro Asn Ala Glu Lys Phe Glu Arg Leu Thr Tyr 180

Asp Glu Val Leu Asp Arg Lys Leu Gly Val Met Asp Leu Thr Ala Ile 200

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Cys Leu Cys Arg Asp Gln Asn Met Pro Leu Arg Val Phe Asn Met Asn
Lys Pro Gly Ala Leu Leu Asn Ile Val Val Gly Gly Ala Glu Gly Thr
                                         235
Leu Ile Glu Glu Gly
                245
<210> 273
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 273
                                                                   31
gcggcggccc atatggctca gcaactgagc g
<210> 274
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 274
gcgcggatcc accetectcg atcagggtg
                                                                   29
<210> 275
<211> 22
<212> PRT
<213> Pseudomonas aeruginosa
<400> 275
Tyr Asp Glu Val Leu Asp Arg Lys Leu Gly Val Met Asp Leu Thr Ala
Ile Cys Leu Cys Arg Asp
             20
<210> 276
<211> 18
<212> PRT
<213> Pseudomonas aeruginosa
<400> 276
Glu Ile Gly Gln Leu Val Gly Ile Gly Val Gln Val Gly Leu Val Ile
                                     10
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Gly Gly
<210> 277
<211> 10
<212> PRT
<213> Pseudomonas aeruginosa
<400> 277
Gly Ala Leu Leu Asn Ile Val Val Gly Gly
<210> 278
<211> 1191
<212> DNA
<213> Staphylococcus aureus
<400> 278
atggctaaaa aaattgtttc tgatttagat cttaaaggta aaacagtcct agtacgtgct 60
gattttaacg tacctttaaa agacggtgaa attactaatg acaaccgtat cgttcaagct 120
ttacctacaa ttcaatacat catcgaacaa ggtggtaaaa tcgtactatt ttcacattta 180
ggtaaagtga aagaagaaag tgataaagca aaattaactt tacgtccagt tgctgaagac 240
ttatctaaga aattagataa agaagttgtt ttcgtaccag aaacacgcgg cgaaaaactt 300
gaagctgcta ttaaagacct taaagaaggc gacgtattat tagttgaaaa tacacgttat 360
gaagatttag acggtaaaaa agaatctaaa aatgatccag aattaggtaa atactgggca 420
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45

- Glu Gln Gly Gly Lys Ile Val Leu Phe Ser His Leu Gly Lys Val Lys 50 55 60
- Glu Glu Ser Asp Lys Ala Lys Leu Thr Leu Arg Pro Val Ala Glu Asp
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- Leu Ser Lys Lys Leu Asp Lys Glu Val Val Phe Val Pro Glu Thr Arg 85 90 95
- Gly Glu Lys Leu Glu Ala Ala Ile Lys Asp Leu Lys Glu Gly Asp Val
- Leu Leu Val Glu Asn Thr Arg Tyr Glu Asp Leu Asp Gly Lys Lys Glu
 115 120 125
- Ser Lys Asn Asp Pro Glu Leu Gly Lys Tyr Trp Ala Ser Leu Gly Asp 130 135 140
- Val Phe Val Asn Asp Ala Phe Gly Thr Ala His Arg Glu His Ala Ser 145 150 155 160
- Asn Val Gly Ile Ser Thr His Leu Glu Thr Ala Ala Gly Phe Leu Met 165 170 175
- Asp Lys Glu Ile Lys Phe Ile Gly Gly Val Val Asn Asp Pro His Lys 180 185 190
- Pro Val Val Ala Ile Leu Gly Gly Ala Lys Val Ser Asp Lys Ile Asn 195 200 205
- Val Ile Lys Asn Leu Val Asn Ile Ala Asp Lys Ile Ile Gly Gly 210 215 220
- Gly Met Ala Tyr Thr Phe Leu Lys Ala Gln Gly Lys Glu Ile Gly Ile 225 230 235 240
- Ser Leu Leu Glu Glu Asp Lys Ile Asp Phe Ala Lys Asp Leu Leu Glu 245 250 255
- Lys His Gly Asp Lys Ile Val Leu Pro Val Asp Thr Lys Val Ala Lys 260 265 270
- Glu Phe Ser Asn Asp Ala Lys Ile Thr Val Val Pro Ser Asp Ser Ile 275 280 285
- Pro Ala Asp Gln Glu Gly Met Asp Ile Gly Pro Asn Thr Val Lys Leu 290 295 300
- Phe Ala Asp Glu Leu Glu Gly Ala His Thr Val Val Trp Asn Gly Pro 305 310 315 320
- Met Gly Val Phe Glu Phe Ser Asn Phe Ala Gln Gly Thr Ile Gly Val 325 330 335
- Cys Lys Ala Ile Ala Asn Leu Lys Asp Ala Ile Thr Ile Ile Gly Gly 340 345 350

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ttacctacaa ttcaatacat catcgaacaa ggtggtaaaa tcgtactatt ttcacattta 180
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Glu Gln Gly Gly Lys Ile Val Leu Phe Ser His Leu Gly Lys Val Lys
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Glu Glu Ser Asp Lys Ala Lys Leu Thr Leu Arg Pro Val Ala Glu Asp
 65
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- Leu Ser Lys Lys Leu Asp Lys Glu Val Val Phe Val Pro Glu Thr Arg 85 90 95

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- Leu Leu Val Glu Asn Thr Arg Tyr Glu Asp Leu Asp Gly Lys Lys Glu 115 120 125
- Ser Lys Asn Asp Pro Glu Leu Gly Lys Tyr Trp Ala Ser Leu Gly Asp
- Val Phe Val Asn Asp Ala Phe Gly Thr Ala His Arg Glu His Ala Ser 145 150 155 160
- Asn Val Gly Ile Ser Thr His Leu Glu Thr Ala Ala Gly Phe Leu Met 165 170 175
- Asp Lys Glu Ile Lys Phe Ile Gly Gly Val Val Asn Asp Pro His Lys 180 185 190
- Pro Val Val Ala Ile Leu Gly Gly Ala Lys Val Ser Asp Lys Ile Asn 195 200 205
- Val Ile Lys Asn Leu Val Asn Ile Ala Asp Lys Ile Ile Gly Gly 210 215 220
- Gly Met Ala Tyr Thr Phe Leu Lys Ala Gln Gly Lys Glu Ile Gly Ile 225 230 235 240
- Ser Leu Leu Glu Glu Asp Lys Ile Asp Phe Ala Lys Asp Leu Leu Glu 245 250 255
- Lys His Gly Asp Lys Ile Val Leu Pro Val Asp Thr Lys Val Ala Lys 260 265 270
- Glu Phe Ser Asn Asp Ala Lys Ile Thr Val Val Pro Ser Asp Ser Ile 275 280 285
- Pro Ala Asp Gln Lys Gly Met Asp Ile Gly Pro Asn Thr Val Lys Leu 290 295 300
- Phe Ala Asp Glu Leu Glu Gly Ala His Thr Val Val Trp Asn Gly Pro 305 310 315 320
- Met Gly Val Phe Glu Phe Ser Asn Phe Ala Gln Gly Thr Ile Gly Val 325 330 335
- Cys Lys Ala Ile Ala Asn Leu Lys Asp Ala Ile Thr Ile Ile Gly Gly 340 345 350
- Gly Asp Ser Ala Ala Ala Ala Ile Ser Leu Gly Phe Glu Asn Asp Phe 355 360 365
- Thr His Ile Ser Thr Gly Gly Gly Ala Ser Leu Glu Tyr Leu Glu Gly 370 375 380

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<213> Artificial Sequence
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Asn Ile Ala Asp Lys Ile Ile Ile
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gctgcctata aaacccctga actggtgcgt cgtttgcgcg atcgcggggc cgacgtccgc 180
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Val Arg Arg Leu Arg Asp Arg Gly Ala Asp Val Arg Val Ala Met Thr
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- Glu Ala Ala Lys Ala Phe Ile Thr Pro Leu Ser Leu Gln Ala Val Ser 65 70 75 80
- Gly Tyr Pro Val Ser Asp Ser Leu Leu Asp Pro Ala Ala Glu Ala Ala 85 90 95
- Met Gly His Ile Glu Leu Gly Lys Trp Ala Asp Leu Val Ile Leu Ala 100 105 110
- Pro Ala Thr Ala Asp Leu Ile Ala Arg Val Ala Ala Gly Met Ala Asn 115 120 125
- Asp Leu Val Ser Thr Ile Cys Leu Ala Thr Pro Ala Pro Val Ala Val 130 135 140
- Leu Pro Ala Met Asn Gln Gln Met Tyr Arg Ala Ala Ala Thr Gln His 145 150 155 160
- Asn Leu Glu Val Leu Ala Ser Arg Gly Leu Leu Ile Trp Gly Pro Asp 165 170 175
- Ser Gly Ser Gln Ala Cys Gly Asp Ile Gly Pro Gly Arg Met Leu Asp 180 185 190
- Pro Leu Thr Ile Val Asp Met Ala Val Ala His Phe Ser Pro Val Asn 195 200 205
- Asp Leu Lys His Leu Asn Ile Met Ile Thr Ala Gly Pro Thr Arg Glu 210 215 220
- Pro Leu Asp Pro Val Arg Tyr Ile Ser Asn His Ser Ser Gly Lys Met 225 230 235 240
- Gly Phe Ala Ile Ala Ala Ala Ala Arg Arg Gly Ala Asn Val Thr 245 250 255
- Leu Val Ser Gly Pro Val Ser Leu Pro Thr Pro Pro Phe Val Lys Arg 260 265 270
- Val Asp Val Met Thr Ala Leu Glu Met Glu Ala Ala Val Asn Ala Ser 275 280 285
- Val Gln Gln Gln Asn Ile Phe Ile Gly Cys Ala Ala Val Ala Asp Tyr 290 295 300
- Arg Ala Ala Thr Val Ala Pro Glu Lys Ile Lys Lys Gln Ala Thr Gln 305 310 315 320
- Gly Asp Glu Leu Thr Ile Lys Met Val Lys Asn Pro Asp Ile Val Ala 325 330 335
- Gly Val Ala Ala Leu Lys Asp His Arg Pro Tyr Val Val Gly Phe Ala 340 345 350
- Ala Glu Thr Asn Asn Val Glu Glu Tyr Ala Arg Gln Lys Arg Ile Arg 355 360 365

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Asp Lys Val Leu Pro Leu Glu Arg Lys Glu Leu Leu Gly Gln Leu Leu
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gataaagtct taccgcttga gcgcaaagag ctccttggcc aattattact cgacgagatc 1260
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Cys His Pro Thr Gly Lys Ile Ile Met Ser Leu Ala Gly Lys Lys Ile
Val Leu Gly Val Ser Gly Gly Ile Ala Ala Tyr Lys Thr Pro Glu Leu
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- Val Arg Arg Leu Arg Asp Arg Gly Ala Asp Val Arg Val Ala Met Thr 50 55 60
- Glu Ala Ala Lys Ala Phe Ile Thr Pro Leu Ser Leu Gln Ala Val Ser 65 70 75 80
- Gly Tyr Pro Val Ser Asp Ser Leu Leu Asp Pro Ala Ala Glu Ala Ala 85 90 95
- Met Gly His Ile Glu Leu Gly Lys Trp Ala Asp Leu Val Ile Leu Ala 100 105 110
- Pro Ala Thr Ala Asp Leu Ile Ala Arg Val Ala Ala Gly Met Ala Asn 115 120 125
- Asp Leu Val Ser Thr Ile Cys Leu Ala Thr Pro Ala Pro Val Ala Val 130 135
- Leu Pro Ala Met Asn Gln Gln Met Tyr Arg Ala Ala Ala Thr Gln His 145 150 155 160
- Asn Leu Glu Val Leu Ala Ser Arg Gly Leu Leu Ile Trp Gly Pro Asp 165 170 175
- Ser Gly Ser Gln Ala Cys Gly Asp Ile Gly Pro Gly Arg Met Leu Asp 180 185 190
- Pro Leu Thr Ile Val Asp Met Ala Val Ala His Phe Ser Pro Val Asn 195 200 205
- Asp Leu Lys His Leu Asn Ile Met Ile Thr Ala Gly Pro Thr Arg Glu 210 215 220
- Pro Leu Asp Pro Val Arg Tyr Ile Ser Asn His Ser Ser Gly Lys Met 225 230 235 235
- Gly Phe Ala Ile Ala Ala Ala Ala Ala Arg Arg Gly Ala Asn Val Thr 245 250 255
- Leu Val Ser Gly Pro Val Ser Leu Pro Thr Pro Pro Phe Val Lys Arg 260 265 270
- Val Asp Val Met Thr Ala Leu Glu Met Glu Ala Ala Val Asn Ala Ser 275 280 285
- Val Gln Gln Gln Asn Ile Phe Ile Gly Cys Ala Ala Val Ala Asp Tyr 290 295 300
- Arg Ala Ala Thr Val Ala Pro Glu Lys Ile Lys Lys Gln Ala Thr Gln 305 310 315 320
- Gly Asp Glu Leu Thr Ile Lys Met Val Lys Asn Pro Asp Ile Val Ala 325 330 335
- Gly Val Ala Ala Leu Lys Asp His Arg Pro Tyr Val Val Gly Phe Ala 340 345 350

Ala Glu Thr Asn Asn Val Glu Glu Tyr Ala Arg Gln Lys Arg Ile Arg Lys Asn Leu Asp Leu Ile Cys Ala Asn Asp Val Ser Gln Pro Thr Gln Gly Phe Asn Ser Asp Asn Asn Ala Leu His Leu Phe Trp Gln Asp Gly 385 390 395 Asp Lys Val Leu Pro Leu Glu Arg Lys Glu Leu Leu Gly Gln Leu Leu Leu Asp Glu Ile Val Thr Arg Tyr Asp Glu Lys Asn Arg Arg 425 <210> 291 <211> 33 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Synthetic primer <400> 291 33 gcggcggccc atatgaaggc acgacaacaa aag <210> 292 <211> 30 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic primer <400> 292 30 gcgcggatcc aacgggataa ccagaaaccg <210> 293 <211> 21 <212> PRT <213> Escherichia coli <400> 293 Asn Asp Leu Val Ser Thr Ile Cys Leu Ala Thr Pro Ala Pro Val Ala 5 10 Val Leu Pro Ala Met

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tataatatct ag
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<211> 323
<212> PRT
<213> Staphylococcus aureus
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 20 25 30
- Gly His Asp Lys Val Phe Asp Ile Leu Asn Glu Ile Ala Glu Ala Arg 35 40 45
- Ser Leu Lys Lys Ala Val Met Thr Phe Asp Pro His Pro Ser Val Val 50 55 60
- Leu Asn Pro Lys Arg Lys Arg Thr Thr Tyr Leu Thr Pro Leu Ser Asp 65 70 75 80
- Lys Ile Glu Lys Ile Ser Gln His Asp Ile Asp Tyr Cys Ile Val Val 85 90 95
- Asn Phe Ser Ser Arg Phe Ala Asn Val Ser Val Glu Asp Phe Val Glu
- Asn Tyr Ile Ile Lys Asn Asn Val Lys Glu Val Ile Ala Gly Phe Asp 115 120 125
- Phe Thr Phe Gly Lys Phe Gly Lys Gly Asn Met Thr Val Leu Gln Glu 130 135 140
- Tyr Asp Ala Phe Asn Thr Thr Ile Val Ser Lys Gln Glu Ile Glu Asn 145 150 155 160
- Glu Lys Ile Ser Thr Thr Ser Ile Arg Gln Asp Leu Ile Asn Gly Glu 165 170 175
- Leu Gln Lys Ala Asn Asp Ala Leu Gly Tyr Ile Tyr Ser Ile Lys Gly
 180 185 190
- Thr Val Val Gln Gly Glu Lys Arg Gly Arg Thr Ile Gly Phe Pro Thr 195 200 205
- Ala Asn Ile Gln Pro Ser Asp Asp Tyr Leu Leu Pro Arg Lys Gly Val 210 215 220
- Tyr Ala Val Ser Ile Glu Ile Gly Thr Glu Asn Lys Leu Tyr Arg Gly 225 230 235 240
- Val Ala Asn Ile Gly Val Lys Pro Thr Phe His Asp Pro Asn Lys Ala 245 250 255
- Glu Val Val Ile Glu Val Asn Ile Phe Asp Phe Glu Asp Asn Ile Tyr 260 265 270
- Gly Glu Arg Val Thr Val Asn Trp His His Phe Leu Arg Pro Glu Ile 275 280 285
- Lys Phe Asp Gly Ile Asp Pro Leu Val Lys Gln Met Asn Asp Asp Lys 290 295 300
- Ser Arg Ala Lys Tyr Leu Leu Ala Val Asp Phe Gly Asp Glu Val Ala 305 310 315 320

Tyr Asn Ile

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gtagctaaca taggtgtaaa gccaacattt catgatccta acaaagcaga agttgtcatc 780
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Thr Glu Asp Val Ala Met Ala Phe Gly Phe Phe Asp Gly Met His Lys
                                 25
Gly His Asp Lys Val Phe Asp Ile Leu Asn Glu Ile Ala Glu Ala Arg
Ser Leu Lys Lys Ala Val Met Thr Phe Asp Pro His Pro Ser Val Val
Leu Asn Pro Lys Arg Lys Arg Thr Thr Tyr Leu Thr Pro Leu Ser Asp
                     70
Lys Ile Glu Lys Ile Ser Gln His Asp Ile Asp Tyr Cys Ile Val Val
Asn Phe Ser Ser Arg Phe Ala Asn Val Ser Val Glu Asp Phe Val Glu
Asn Tyr Ile Ile Lys Asn Asn Val Lys Glu Val Ile Ala Gly Phe Asp
                            120
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Phe Thr Phe Gly Lys Phe Gly Lys Gly Asn Met Thr Val Leu Gln Glu 130 135 140

Tyr Asp Ala Phe Asn Thr Thr Ile Val Ser Lys Gln Glu Ile Glu Asn 145 150 155 160

Glu Lys Ile Ser Thr Thr Ser Ile Arg Gln Asp Leu Ile Asn Gly Glu 165 170 175

Leu Gln Lys Ala Asn Asp Ala Leu Gly Tyr Ile Tyr Ser Ile Lys Gly
180 185 190

Thr Val Val Gln Gly Glu Lys Arg Gly Arg Thr Ile Gly Phe Pro Thr 195 200 205

Ala Asn Ile Gln Pro Ser Asp Asp Tyr Leu Leu Pro Arg Lys Gly Val 210 215 220

Tyr Ala Val Ser Ile Glu Ile Gly Thr Glu Asn Lys Leu Tyr Arg Gly 225 230 235 240

Val Ala Asn Ile Gly Val Lys Pro Thr Phe His Asp Pro Asn Lys Ala 245 250 255

Glu Val Val Ile Glu Val Asn Ile Phe Asp Phe Glu Asp Asn Ile Tyr 260 265 270

Gly Glu Arg Val Thr Val Asn Trp His His Phe Leu Arg Pro Glu Ile 275 280 285

Lys Phe Asp Gly Ile Asp Pro Leu Val Lys Gln Met Asn Asp Asp Lys 290 295 300

Ser Arg Ala Lys Tyr Leu Leu Ala Val Asp Phe Gly Asp Glu Val Ala 305 310 315 320

Tyr Asn Ile

<210> 300

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 300

gcggcggccc atatgaaagt catagaagtg acac

34

<210> 301

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
      primer
<400> 301
gcgcggatcc tttttcgatt ttatctgaaa gtg
                                                                   33
<210> 302
<211> 13
<212> PRT
<213> Staphylococcus aureus
<400> 302
Gln His Asp Ile Asp Tyr Cys Ile Val Val Asn Phe Ser
<210> 303
<211> 9
<212> PRT
<213> Staphylococcus aureus
<400> 303
Pro His Pro Ser Val Val Leu Asn Pro
<210> 304
<211> 8
<212> PRT
<213> Staphylococcus aureus
<400> 304
Ala Lys Tyr Leu Leu Ala Val Asp
<210> 305
<211> 480
<212> DNA
<213> Pseudomonas aeruginosa
<400> 305
atgaaccgag tgctgtaccc aggcaccttc qatcccatca ccaaqqqtca cqqcqatctq 60
ategaaegtg etteaegget tttegaeeat gtgateateg eggtegeege eageeeeaag 120
aagaaccccc tgttcagcct ggaacagcgg gttgcgctgg cccaggaggt caccaagcac 180
ctgccgaacg tcgaggtggt gggcttctcc accetgctgg cgcacttcgt caaggagcag 240
aaggcgaatg tetteeteeg eggeetgege geggttteeg aettegagta egagtteeag 300
ctggccaaca tgaaccgcca gctcgcccc gacgtggaaa gcatgttcct caccccgtcg 360
gagaagtatt cetteattte etegacgetg gteegggaaa tegeegetet eggeggggat 420
atcagcaagt tcgtgcatcc ggccgtggca gacgccctgg cggaacgttt caagcgctga 480
<210> 306
<211> 159
<212> PRT
<213> Pseudomonas aeruginosa
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<400> 306
Met Asn Arg Val Leu Tyr Pro Gly Thr Phe Asp Pro Ile Thr Lys Gly
His Gly Asp Leu Ile Glu Arg Ala Ser Arg Leu Phe Asp His Val Ile
Ile Ala Val Ala Ala Ser Pro Lys Lys Asn Pro Leu Phe Ser Leu Glu
                             40
                                                 45
Gln Arg Val Ala Leu Ala Gln Glu Val Thr Lys His Leu Pro Asn Val
Glu Val Val Gly Phe Ser Thr Leu Leu Ala His Phe Val Lys Glu Gln
                     70
Lys Ala Asn Val Phe Leu Arg Gly Leu Arg Ala Val Ser Asp Phe Glu
Tyr Glu Phe Gln Leu Ala Asn Met Asn Arg Gln Leu Ala Pro Asp Val
            100
                                105
Glu Ser Met Phe Leu Thr Pro Ser Glu Lys Tyr Ser Phe Ile Ser Ser
Thr Leu Val Arg Glu Ile Ala Ala Leu Gly Gly Asp Ile Ser Lys Phe
Val His Pro Ala Val Ala Asp Ala Leu Ala Glu Arg Phe Lys Arg
                    150
                                        155
<210> 307
<211> 480
<212> DNA
<213> Pseudomonas aeruginosa
<400> 307
atgaaccgag tgctgtaccc aggcaccttc gatcccatca ccaagggtca cggcgatctg 60
ategaacgtg cttcacggct tttcgaccat gtgatcatcg cggtcgccgc cagccccaag 120
aagaaccccc tgttcagcct ggaacagcgg gtggcgctgg cccaggaggt caccaagcac 180
ctgccgaacg tcgaggtggt gggcttctcc accctgctgg cgcacttcgt caaggagcag 240
aaggegaatg tetteeteeg eggeetgege geggttteeg acttegagta egagtteeag 300
ctggccaaca tgaaccgcca gctcgcccc gacgtggaaa gcatgttcct caccccgtcg 360
gagaagtatt ccttcatttc ctcgacgctg gtccgggaaa tcgccgctct cggcggggat 420
atcagcaagt tegtgeatee ggeegtggea gaegeeetgg eggaaegttt caagegetga 480
<210> 308
<211> 159
<212> PRT
<213> Pseudomonas aeruginosa
<400> 308
Met Asn Arg Val Leu Tyr Pro Gly Thr Phe Asp Pro Ile Thr Lys Gly
                                     10
```

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His Gly Asp Leu Ile Glu Arg Ala Ser Arg Leu Phe Asp His Val Ile
                                 25
Ile Ala Val Ala Ala Ser Pro Lys Lys Asn Pro Leu Phe Ser Leu Glu
Gln Arg Val Ala Leu Ala Gln Glu Val Thr Lys His Leu Pro Asn Val
Glu Val Val Gly Phe Ser Thr Leu Leu Ala His Phe Val Lys Glu Gln
Lys Ala Asn Val Phe Leu Arg Gly Leu Arg Ala Val Ser Asp Phe Glu
Tyr Glu Phe Gln Leu Ala Asn Met Asn Arg Gln Leu Ala Pro Asp Val
Glu Ser Met Phe Leu Thr Pro Ser Glu Lys Tyr Ser Phe Ile Ser Ser
        115
                            120
Thr Leu Val Arg Glu Ile Ala Ala Leu Gly Gly Asp Ile Ser Lys Phe
Val His Pro Ala Val Ala Asp Ala Leu Ala Glu Arg Phe Lys Arg
<210> 309
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 309
gcggcggccc atatgaaccg agtgctgtac c
                                                                   31
<210> 310
<211> 28
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
      primer
<400> 310
gcgcggatcc gcgcttgaaa cgttccgc
                                                                   28
<210> 311
<211> 17
<212> PRT
<213> Pseudomonas aeruginosa
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```
<400> 311
Glu Arg Ala Ser Arg Leu Phe Asp His Val Ile Ile Ala Val Ala Ala
                  5
Ser
<210> 312
<211> 14
<212> PRT
<213> Pseudomonas aeruginosa
<400> 312
Ser Lys Phe Val His Pro Ala Val Ala Asp Ala Leu Ala Glu
<210> 313
<211> 39
<212> PRT
<213> Pseudomonas aeruginosa
<400> 313
Lys Asn Pro Leu Phe Ser Leu Glu Gln Arg Val Ala Leu Ala Gln Glu
Val Thr Lys His Leu Pro Asn Val Glu Val Val Gly Phe Ser Thr Leu
             20
                                 25
Leu Ala His Phe Val Lys Glu
<210> 314
<211> 1083
<212> DNA
<213> Pseudomonas aeruginosa
<400> 314
atgaaagett etetgetgaa aaagetggat gteeteageg ategetaega agaaetgaeg 60
gegetgeteg gegaegeega ggtgateagt gaceagaeee getteegege etatteeege 120
gagtacgccg aggtcgaacc ggtgatcctg gcgttccgcg actaccgcaa ggtgcaggcc 180
gacctcgagg gcgcccaggc gttgctcaag gacagcgacc cqqaqttqcq cqacctcqcc 240
gaggaggagg tegeegaage gegeggeege etegeegeee teggegaeag eetgeagege 300
atgetgetge egaaggatee caaegacage egeaaegtgt teetggagat eegtgeegge 360
accggtggcg acgaggcggc gatettetee ggcgacetgt teegcatgta ttegegetae 420
gccgagcgcc agggctggcg gatcgagacg ctgtcggaga acgagggcga gcacggtggc 480
tacaaggaag tgattgcccg ggtcgagggc gacaacgtct acgccaagct caagttcgag 540
teeggegege accgegtgea gegggtgeeg gaaaccgaat ceeagggeeg gatecacact 600
teegeetgea eegtegeggt getgeeggag eeggaegage aggeagegat egagateaac 660
ceggeegace tgegggtgga cacetacegt teeteeggtg ceggeggeea geaegteaac 720
aagaccgact cggcggtgcg catcacccac attcccagcg gcatcgtggt cgagtgccag 780
gaagageget egeageacaa gaacegegee aaggecatgg eetggetgge ggecaagete 840
aacgaccage agcaggeege ggegeageag gegategeea geaegegeaa getgetggtg 900
ggctcgggcg accgctcgga gcgcatccgt acctacaact tcccgcaagg gcgggtcacc 960
gaccategea teaaceteae cetgtaetee etgggegagg tgatggaggg egeggtggaa 1020
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caggtgatcg agccgctgct gcaggaatac caggccgatc aactggcggc cctgggcgac 1080 tga

<210> 315

<211> 360

<212> PRT

<213> Pseudomonas aeruginosa

<400> 315

Met Lys Ala Ser Leu Leu Lys Lys Leu Asp Val Leu Ser Asp Arg Tyr

1 10 15

Glu Glu Leu Thr Ala Leu Leu Gly Asp Ala Glu Val Ile Ser Asp Gln
20 25 30

Thr Arg Phe Arg Ala Tyr Ser Arg Glu Tyr Ala Glu Val Glu Pro Val
35 40 45

Ile Leu Ala Phe Arg Asp Tyr Arg Lys Val Gln Ala Asp Leu Glu Gly
50 55 60

Ala Gln Ala Leu Leu Lys Asp Ser Asp Pro Glu Leu Arg Asp Leu Ala 65 70 75 80

Glu Glu Val Ala Glu Ala Arg Gly Arg Leu Ala Ala Leu Gly Asp
85
90
95

Ser Leu Gln Arg Met Leu Leu Pro Lys Asp Pro Asn Asp Ser Arg Asn 100 105 110

Val Phe Leu Glu Ile Arg Ala Gly Thr Gly Gly Asp Glu Ala Ile 115 120 125

Phe Ser Gly Asp Leu Phe Arg Met Tyr Ser Arg Tyr Ala Glu Arg Gln 130 135 140

Gly Trp Arg Ile Glu Thr Leu Ser Glu Asn Glu Gly Glu His Gly Gly 145 150 155 160

Tyr Lys Glu Val Ile Ala Arg Val Glu Gly Asp Asn Val Tyr Ala Lys 165 170 175

Leu Lys Phe Glu Ser Gly Ala His Arg Val Gln Arg Val Pro Glu Thr
180 185 190

Glu Ser Gln Gly Arg Ile His Thr Ser Ala Cys Thr Val Ala Val Leu 195 200 205

Pro Glu Pro Asp Glu Gln Ala Ala Ile Glu Ile Asn Pro Ala Asp Leu 210 215 220

Arg Val Asp Thr Tyr Arg Ser Ser Gly Ala Gly Gly Gln His Val Asn 225 230 235 240

Lys Thr Asp Ser Ala Val Arg Ile Thr His Ile Pro Ser Gly Ile Val 245 250 255

```
Val Glu Cys Gln Glu Glu Arg Ser Gln His Lys Asn Arg Ala Lys Ala
            260
                                265
Met Ala Trp Leu Ala Ala Lys Leu Asn Asp Gln Gln Ala Ala Ala
                            280
Gln Gln Ala Ile Ala Ser Thr Arg Lys Leu Leu Val Gly Ser Gly Asp
                        295
Arg Ser Glu Arg Ile Arg Thr Tyr Asn Phe Pro Gln Gly Arg Val Thr
                    310
                                        315
Asp His Arg Ile Asn Leu Thr Leu Tyr Ser Leu Gly Glu Val Met Glu
Gly Ala Val Glu Gln Val Ile Glu Pro Leu Leu Gln Glu Tyr Gln Ala
                                345
Asp Gln Leu Ala Ala Leu Gly Asp
        355
                            360
<210> 316
<211> 1083
<212> DNA
<213> Pseudomonas aeruginosa
<400> 316
atgaaagett etetgetgaa aaagetggat gteeteageg ategetaega agaactgaeg 60
gcgctgctcg gcgacgccga ggtgatcagt gaccagaccc gcttccgcgc ctattcccgc 120
gagtacgccg aggtcgaacc gttgatcctg gagttccgcg actaccgcaa ggtgcaggcc 180
gacctcgagg gcgcccaggc gttgctcaag gacagcgacc cggagttgcg cgacctcgcc 240
gaggaggagg tegeegaage gegeggeege etegeegeee teggegaeag cetgeagege 300
atgctgctgc cgaaggatcc caacgacagc cgcaacgtgt tcctggagat ccgtgccggc 360
acceggtggcg acgaggcggc gatcttctcc ggcgacctgt tccgcatgta ttcgcgctac 420
gccgagcgcc agggctggcg gatcgagacg ctgtcggaga acgagggcga gcacggtggc 480
tacaaggaag tgattgcccg ggtcgagggc gacaacgtct acgccaagct caagttcgag 540
teeggegege accegegtgea gegggtgeeg gaaaccgaat ceeagggeeg gatecacact 600
teegeetgea eegtegeggt getgeeggag eeggaegage aggeagegat egagateaac 660
ccggccgacc tgcgggtgga cacctaccgt tcctccggtg ccggcggcca gcacgtcaac 720
aagaccgact cggcggtgcg catcacccac attcccagcg gcatcgtggt cgagtgccag 780
gaagageget egeageaeaa gaacegegee aaggeeatgg cetggetgge ggeeaagete 840
aacgaccagc agcaggccgc ggcgcagcag gcgatcgcca gcacgcgcaa gctgctggtg 900
qqctcqqqcq tccqctcqqa qcqcatccqt acctacaact tcccgcaagg gcgggtcacc 960
qaccatcqca tcaacctcac cctqtactcc ctgggcgagg tgatggaggg cgcggtggaa 1020
caggtgatcg agccgctgct gcaggaatac caggccgatc aactggcggc cctgggcgac 1080
                                                                   1083
tga
<210> 317
<211> 360
<212> PRT
<213> Pseudomonas aeruginosa
<400> 317
Met Lys Ala Ser Leu Leu Lys Lys Leu Asp Val Leu Ser Asp Arg Tyr
```

- Glu Glu Leu Thr Ala Leu Leu Gly Asp Ala Glu Val Ile Ser Asp Gln
 20 25 30
- Thr Arg Phe Arg Ala Tyr Ser Arg Glu Tyr Ala Glu Val Glu Pro Leu 35 40 45
- Ile Leu Glu Phe Arg Asp Tyr Arg Lys Val Gln Ala Asp Leu Glu Gly 50 55 60
- Ala Gln Ala Leu Leu Lys Asp Ser Asp Pro Glu Leu Arg Asp Leu Ala 65 70 75 80
- Glu Glu Glu Val Ala Glu Ala Arg Gly Arg Leu Ala Ala Leu Gly Asp 85 90 95
- Ser Leu Gln Arg Met Leu Leu Pro Lys Asp Pro Asn Asp Ser Arg Asn 100 105 110
- Val Phe Leu Glu Ile Arg Ala Gly Thr Gly Gly Asp Glu Ala Ala Ile 115 120 125
- Phe Ser Gly Asp Leu Phe Arg Met Tyr Ser Arg Tyr Ala Glu Arg Gln 130 135 140
- Gly Trp Arg Ile Glu Thr Leu Ser Glu Asn Glu Gly Glu His Gly Gly 145 150 155 160
- Tyr Lys Glu Val Ile Ala Arg Val Glu Gly Asp Asn Val Tyr Ala Lys 165 170 175
- Leu Lys Phe Glu Ser Gly Ala His Arg Val Gln Arg Val Pro Glu Thr 180 185 190
- Glu Ser Gln Gly Arg Ile His Thr Ser Ala Cys Thr Val Ala Val Leu 195 200 205
- Pro Glu Pro Asp Glu Gln Ala Ala Ile Glu Ile Asn Pro Ala Asp Leu 210 215 220
- Arg Val Asp Thr Tyr Arg Ser Ser Gly Ala Gly Gly Gln His Val Asn 225 230 235 240
- Lys Thr Asp Ser Ala Val Arg Ile Thr His Ile Pro Ser Gly Ile Val 245 250 255
- Val Glu Cys Gln Glu Glu Arg Ser Gln His Lys Asn Arg Ala Lys Ala 260 265 270
- Met Ala Trp Leu Ala Ala Lys Leu Asn Asp Gln Gln Gln Ala Ala Ala 275 280 285
- Gln Gln Ala Ile Ala Ser Thr Arg Lys Leu Leu Val Gly Ser Gly Val 290 295 300
- Arg Ser Glu Arg Ile Arg Thr Tyr Asn Phe Pro Gln Gly Arg Val Thr 305 310 315 320

```
Asp His Arg Ile Asn Leu Thr Leu Tyr Ser Leu Gly Glu Val Met Glu
Gly Ala Val Glu Gln Val Ile Glu Pro Leu Gln Glu Tyr Gln Ala
                               345
Asp Gln Leu Ala Ala Leu Gly Asp
        355
<210> 318
<211> 36
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     primer
<400> 318
gcggcggccc atatgaaagc ttctctgctg aaaaag
                                                                 36
<210> 319
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     primer
<400> 319
gcgcagatct gtcgcccagg gccgcc
                                                                 26
<210> 320
<211> 11
<212> PRT
<213> Pseudomonas aeruginosa
<400> 320
Thr Ser Ala Cys Thr Val Ala Val Leu Pro Glu
1 5
<210> 321
<211> 12
<212> PRT
<213> Pseudomonas aeruginosa
<400> 321
Tyr Ala Glu Val Glu Pro Val Ile Leu Ala Phe Arg
```

```
<210> 322
<211> 17
<212> PRT
<213> Pseudomonas aeruginosa
<400> 322
Ser Ala Val Arg Ile Thr His Ile Pro Ser Gly Ile Val Val Glu Cys
                  5
                                     10
Gln
<210> 323
<211> 10
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     peptide motif
<220>
<221> MOD_RES
<222> (3)
<223> Ile or Met
<400> 323
Gly Val Xaa Val Ser Ala Ser His Asn Pro
                 5
<210> 324
<211> 7
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     peptide motif
<220>
<221> MOD RES
<222> (2)
<223> Gly or Ser
<220>
<221> MOD RES
<222> (5)
<223> Variable amino acid
<400> 324
Gly Xaa Ile Ala Xaa Tyr Lys
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<210> 325
<211> 6
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      6xHis tag
<400> 325
His His His His His
 1
                  5
<210> 326
<211> 4
<212> PRT
<213> Staphylococcus aureus
<400> 326
Met Glu Cys Ile
 1
<210> 327
<211> 6
<212> PRT
<213> Staphylococcus aureus
<400> 327
Met Glu Cys Ile Lys Met
 1
<210> 328
<211> 8
<212> PRT
<213> Staphylococcus aureus
<400> 328
Met Glu Cys Ile Lys Met Leu Asn
 1
<210> 329
<211> 10
<212> PRT
<213> Staphylococcus aureus
<400> 329
Met Glu Cys Ile Lys Met Leu Asn Tyr Thr
<210> 330
<211> 9
<212> PRT
<213> Staphylococcus aureus
```

```
<400> 330
Met Glu Cys Ile Lys Met Leu Asn Tyr
 1 5
<210> 331
<211> 15
<212> PRT
<213> Staphylococcus aureus
Met Glu Cys Ile Lys Met Leu Asn Tyr Thr Gly Leu Glu Asn Lys
                 5
<210> 332
<211> 15
<212> PRT
<213> Staphylococcus aureus
<400> 332
Gly Glu Lys Phe Ile Glu Arg Phe Arg Ala His Leu Pro Ser Tyr
                                    10
<210> 333
<211> 13
<212> PRT
<213> Staphylococcus aureus
<400> 333
Lys Phe Ile Glu Arg Phe Arg Ala His Leu Pro Ser Tyr
<210> 334
<211> 11
<212> PRT
<213> Staphylococcus aureus
<400> 334
Ile Glu Arg Phe Arg Ala His Leu Pro Ser Tyr
<210> 335
<211> 9
<212> PRT
<213> Staphylococcus aureus
<400> 335
Arg Phe Arg Ala His Leu Pro Ser Tyr
```

```
<210> 336
<211> 8
<212> PRT
<213> Staphylococcus aureus
<400> 336
Phe Arg Ala His Leu Pro Ser Tyr
 1
                5
<210> 337
<211> 5
<212> PRT
<213> Staphylococcus aureus
<400> 337
His Leu Pro Ser Tyr
 1
<210> 338
<211> 4
<212> PRT
<213> Staphylococcus aureus
<400> 338
Met Ser Lys Glu
 1
<210> 339
<211> 6
<212> PRT
<213> Staphylococcus aureus
<400> 339
Met Ser Lys Glu Phe Tyr
 1
<210> 340
<211> 8
<212> PRT
<213> Staphylococcus aureus
<400> 340
Met Ser Lys Glu Phe Tyr Ile Met
1 5
<210> 341
<211> 10
<212> PRT
<213> Staphylococcus aureus
Met Ser Lys Glu Phe Tyr Ile Met Thr His
                5
```

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<210> 342
<211> 4
<212> PRT
<213> Staphylococcus aureus
<400> 342
Lys Asn Ala Phe
1
<210> 343
<211> 6
<212> PRT
<213> Staphylococcus aureus
<400> 343
Gly Met Lys Asn Ala Phe
<210> 344
<211> 8
<212> PRT
<213> Staphylococcus aureus
<400> 344
Lys Leu Gly Met Lys Asn Ala Phe
1
<210> 345
<211> 10
<212> PRT
<213> Staphylococcus aureus
<400> 345
Leu Asp Lys Leu Gly Met Lys Asn Ala Phe
<210> 346
<211> 4
<212> PRT
<213> Streptococcus pneumoniae
<400> 346
Met Gly Lys Tyr
1
<210> 347
<211> 6
<212> PRT
<213> Streptococcus pneumoniae
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```
<400> 347
Met Gly Lys Tyr Phe Gly
<210> 348
<211> 8
<212> PRT
<213> Streptococcus pneumoniae
<400> 348
Met Gly Lys Tyr Phe Gly Thr Asp
<210> 349
<211> 10
<212> PRT
<213> Streptococcus pneumoniae
<400> 349
Met Gly Lys Tyr Phe Gly Thr Asp Gly Val
<210> 350
<211> 10
<212> PRT
<213> Streptococcus pneumoniae
<400> 350
Asp Val Val Arg Ala Glu Ile Gly Ile Asp
<210> 351
<211> 8
<212> PRT
<213> Streptococcus pneumoniae
<400> 351
Val Arg Ala Glu Ile Gly Ile Asp
<210> 352
<211> 6
<212> PRT
<213> Streptococcus pneumoniae
<400> 352
Ala Glu Ile Gly Ile Asp
```

```
<210> 353
<211> 4
<212> PRT
<213> Streptococcus pneumoniae
<400> 353
Ile Gly Ile Asp
 1
<210> 354
<211> 10
<212> PRT
<213> Streptococcus pneumoniae
<400> 354
Met Lys Val Ile Asp Gln Phe Lys Asn Lys
<210> 355
<211> 7
<212> PRT
<213> Streptococcus pneumoniae
<400> 355
Met Lys Val Ile Asp Gln Phe
1
<210> 356
<211> 13
<212> PRT
<213> Streptococcus pneumoniae
<400> 356
Met Lys Val Ile Asp Gln Phe Lys Asn Lys Lys Val Leu
<210> 357
<211> 4
<212> PRT
<213> Streptococcus pneumoniae
<400> 357
Met Lys Val Ile
 1
<210> 358
<211> 8
<212> PRT
<213> Streptococcus pneumoniae
<400> 358
Met Lys Val Ile Asp Gln Phe Lys
                 5
```

```
<210> 359
<211> 10
<212> PRT
<213> Streptococcus pneumoniae
<400> 359
Phe Ile Asp Thr Val Ala Glu Leu Lys Glu
                  5
<210> 360
<211> 8
<212> PRT
<213> Streptococcus pneumoniae
<400> 360
Asp Thr Val Ala Glu Leu Lys Glu
                 5
<210> 361
<211> 6
<212> PRT
<213> Streptococcus pneumoniae
<400> 361
Val Ala Glu Leu Lys Glu
 1
<210> 362
<211> 4
<212> PRT
<213> Streptococcus pneumoniae
<400> 362
Glu Leu Lys Glu
 1
<210> 363
<211> 4
<212> PRT
<213> Streptococcus pneumoniae
<400> 363
Val Lys Met Ala
1
<210> 364
<211> 6
<212> PRT
<213> Streptococcus pneumoniae
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.

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<400> 364
Val Lys Met Ala Asn Pro
<210> 365
<211> 8
<212> PRT
<213> Streptococcus pneumoniae
<400> 365
Val Lys Met Ala Asn Pro Lys Tyr
<210> 366
<211> 10
<212> PRT
<213> Streptococcus pneumoniae
<400> 366
Val Lys Met Ala Asn Pro Lys Tyr Lys Arg
<210> 367
<211> 13
<212> PRT
<213> Streptococcus pneumoniae
<400> 367
Val Lys Met Ala Asn Pro Lys Tyr Lys Arg Ile Leu Ile
                  5
<210> 368
<211> 10
<212> PRT
<213> Streptococcus pneumoniae
Thr Val Ser Asn Asn Ile Glu Glu Lys Glu
<210> 369
<211> 8
<212> PRT
<213> Streptococcus pneumoniae
<400> 369
Ser Asn Asn Ile Glu Glu Lys Glu
```

```
<210> 370
<211> 6
<212> PRT
<213> Streptococcus pneumoniae
<400> 370
Asn Ile Glu Glu Lys Glu
                 5
 1
<210> 371
<211> 4
<212> PRT
<213> Streptococcus pneumoniae
<400> 371
Glu Glu Lys Glu
 1
<210> 372
<211> 13
<212> PRT
<213> Streptococcus pneumoniae
<400> 372
Ile Gly Thr Thr Val Ser Asn Asn Ile Glu Glu Lys Glu
 1
                  5
                                      10
```

3

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